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Match Length DB

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Description

A63255 HSILL3REC

A63255 Sequence 1 X95302 H.saptens m Y08768 H.saptens m I81220 Sequence 3 U70981 Human inter

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AB020862 Homo sapi AC006279 Plasmodiu AC004106 Homo sapi U15127 Escherichia

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M33862 Dictyosteli AC007435 Homo sapi

AF044502 Escherich Continuation (4 of AF016443 Caenorhab

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Number of hits that pass the threshold
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298547 Plasmodium
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AC002449 Human PAC
U39994 Caenorhabdi
AC007446 Homo sapi
U40418 Caenorhabdi
U26736 Caenorhabdi
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Other publication AU 757596 19970627 Other publication FR 2742176 19970613. Location/Qualifiers	CHOULD:, RETEATA, P., LEATERT, P., VITA AND NATALIO JI. J. RECEPTOR POLYPEPTILE FILENC: WO 9720926-1 I 12-JUN-1997; SANOET SA (FR)	unicentified urclassified. 1 (bases 1 to 1539)	. unidentified.	Sequence 1 from Paten' W09720926	'A60055' 1539 bp DN0
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	J. Biol. Chem. 271 (28), 16921-16926 (1996) 96279273	JOURNAL MEDLINE	
-13 lpha	ng and characterization of a specific interleukin (IL)	TITLE	بتغو
ta, N.	Laurent,P., Kaghad,M., Lelias,J.M., Lefort,S., Vi a,P.	AUTHORS	g Fire
à	Metazoa; Chordata; Vertebrata; Mammalia; Eutheri Catarrhini; Hominidae; Homo. 1 to 1988	RENCE	
	ons	SOURCE	
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9	HSILISEC 198 DP MKNA PRI 07-AUG-19 H.sapiens mRNA for IL13 receptor. X95302	DEFINITION ACCESSION	, ~ = =
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1500 1500	tttccatatcaagagacatggtattgactcaacagtttccagtcatggccaaatgttcaa 	Qy · 1441 Db · 1441	
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1380	TTTCATCTTAATATTAGTTATATTTGTAACCGGTCTGCTTAGTGAATGTTGCGTAAGCC	1321	.
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0; Mismatches 0; Indels 24
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HSIL13 1376 bp mRNA PRI 05- H.sapters mRNA for IL-13 receptor. Y08768 91877211 Y08768.1 GI:1877211 IL-13 receptor. human. Homo sapiens Eukarycta; Metazoa; Chordata; Vertebrata; Mammalia; E	Ett.catatcaagayacatggtattgactcaacagtttccagt.catggccaaatgtt	gff*catcttaatattagttatatttgtaacoggtctgcttagtgaatgttgcgtaa i	aga:yacggaatt:gggcaaagaatcaagtagtggagtggagtgataaacaatgct :: : : : : : : : : : : :	gtgact/octacagttgaaaatgaaacatac 	tgaaattaagotgaaatggagoatacotttgtttaggogtggacotattocagoaag	aacaagcctgaaatatcaaggaatcagatccagttatttcacttttcagcttcaaaatat	. ttgattacatcaaggottgatggacaaaatataggatgcagatttccctatttggca	ZABOTTGTTTACTGGTATGAGGGCTTGGATCATGCATTACACAC
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Oy 302 aataccgaaacattggtagtgaaacatggaaggctagtgtagagggttaccatcattacta 361	Qy 122 acaagcttttgcacttcatcttcagacaccgagataaaagttaaccctcctcaggatttt 181 Db 192ACTTCATCTTCAGACACCGAGATAAAAGTTAACCCTCCTCAGGATTTT 239 Qy 182 gagatagtggattatgaagagaaccggatacttaggttatcttatttgcaatggaacc 241	Query Match 55.6%; Score 856; DB 9; Length 1376; Best Local Similarity 84.3%; Pred. No. 3.8e-173; Matches 1297; Conservative 0; Mismatches 0; Indels 241; Gaps 20; Qy 2 gtgcctgtcggcggggagagaggcaatatcaaggttttaaatctcggagaaatggcttaa 61	/product="IL-13 receptor" /product="IL-13 receptor" /protein_id="CAA70021.1" /db_xref="PID:e391909" /db_xref="PID:e31877212" /db_xref="SIIS-SPROT:914627" /db_xref="SIIS-PROT:914627" /db_xref="SIIS-PROT:914627" /db_xref="SIIS-PROT:914627" /translation="MAFYCLAIGCLYTFLISTTFGCTSSDTEIKVNPPQDFEIVDPG /translation="MAFYCLAIGCLYTFLISTTFGCTSSDTEIKVNPPQDFEIVDPG /translation="MAFYCLAIGCLYTFLISTTFGCTSSDTEIKVNPPQDFEIVDPG /translation="MAFYCLAIGCLYTFLISTTFGCTSSDTEIKVNPPQDFEIVDPG /translation="MAFYCLAIGCLYTFLISTTFGCTSSDTEIKVNPPQTLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTYWAYLLCSWCFWQYLLCSWKPG /translation="MAFYCLAIGCLYTFLITYTFTIGLTTFGCTSSDTEIKWASIPLGFFILTUTAICSWCFWGFG /translation="MAFYCLAIGCLYTFLITYTGTLLKFWTYSSDTEIKWASIPLGFFILTION="MAFYCLAIGCLYTT" /db_xref="SII-2" /translation="MAFYCLAIGCLYTFLITYTGTLLKFWTYSSDTEIKWASIPLGFFILTION="MAFYCLAIGCLYTT" /translation="MAFYCLAIGCLYTFLITYTGTLLKFWTYSKWTYCSDDGTWGFWGFGSS /translation="MAFYCLAIGCLYTFT" /db_xref="SII-2" /translation="MAFYCLAIGCLYTFLITYTGTLLKFWTYTSKWTYCWGYLLT" /translation="MAFYCLAIGCLYTFLITYTGTLLKFWTYTSSDTEIKWASIPLGFTUTDFG /translation="MAFYCLAIGCLYTFLITYTGTLLT" /translation="MAFYCLAIGCLYTT" /translation="MAFYCLAIGCLYT" /translation="MAFYCLAIGCLYT" /translation="MAFYCLAIGCLYT" /translation="MAFYCL	Biologie, 9 Quai De Moncousu, 44035 Nantes, FRANCE Location/Qualifiers 1. 1376 /organism="Homo sapiens" /db_xref="taxon:9606" /dev_stage="infant" /tissue_type="brain" 126. 1268	., Lebeau.B., lon of the hu)) vielle, Inser
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/dev_stage="ages 22-61 years"
/note="pooled from 4 Caucasians"
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                                                                                atgcattaaatatatttggaaacagtgtgttgattacatcaaggctgatggacaaaatat 751
                                                                                                                                                                                              atgtctgggtacttcttgataccaattacaacttgttttactggtatgaggcttggatc
---agacagTaTaTTCTGATACCAACTATACCATGTTTTCTGGTATGAGGGCTTGGATC
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                                                                                                                                                                                                                                                                                                                          atatcaccacaaggaattccagaaactaaagttcaggattaagttttgggtagaatggat 571
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tctatattttgtgttaatggatcatcatcagagaacaagcctgaaatatcaaaggaatcagatcc
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                           TTTTTATCTGTGTTAATGGATCTTCAAAGTTGGAACCC-----
                                                                                                                                        ATGCCTT-----ACAGTGTGCTGATTACCTCCAGCATGATGAAAAAAATGT
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Collins,M., Donaldson,D., Fitz,L.,
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t: US 5710023-A 1 20-JAN-1998;
Location/Qualifiers
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Submitted (31-JUL-1996) Molecular Immunology, Genetics Institute,
87 CambridgePark Dr., Cambridge, MA 02140, USA
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I (bases 1 to 1567)
Drinaldson, D.D. Whitters, M.J., Fi
Benderson, S.L., O'Hara, R.M. Jr.,
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                                                                                                       /product="IL-13 receptor alpha 2"
/product="IL-13 receptor alpha 2"
/product="IL-13 receptor alpha 2"
/protein id="AAC33240.1"
/db_xref="PID:93483094"
/db_xref="PID:93483094"
/db_xref="GI:3483094"
/translation="MAFVHIRCLCFILLCTITGYSLEIKYNNPPQDFEILDPGLLGYLY
/CHARTSTONE TO THE TO THE
                                                          WESATDKNDMKLKRRANESEDLCFFVRCKVNIYCADDGIWSEWSEEECWEGYTGPDSK
IIFIVPVCLFFIFLLLLLCLIVEKEEPEPTLSLHVDLNKEVCAYEDTLC"
                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/dev_stage="8 wk"
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/strain="C3H/HeJ"
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Dictyostelium discoideum Eukaryota; Dictyosteliida; 1 (bases 1028 to 2982)
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                                spore germination-specific protein.
Dictyosteliu discoideum (strain AX-3) cDNA
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Dorner, F., Scheiflinger, F. and Falkner, F.
Recombinant fowlpox virus
Patent: US 5670367-A:14 23-SEP-1997;
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Sequence 14 from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-JUL-1995) David R. Shaw,
Biology, 340 Kingsland Street, Nutley,
On Aug 1, 1995 this sequence version re
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giorda,R., Ohmachi,T., Shaw,D.R. and Ennis,H.L. A shared internal threonine-glutamic acid-threonine-proline repeat defines a family of Dictyostelium discoideum spore germination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-APR-1990) Herbert L. Ennis, Roche Institute of
Molecular Biology, 340 Kingsland Street, Nutley, NJ 07110-1150, USA
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Sfytsdgnshdvkssdgsvsssyfsgsltnpgifkvtltkegnieftssydeglsati
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SE I ETPTPT ETDTPTPT PSSSSSEGSGSSSETQPP I TPPPTTGTSCLAQVQQKV I NSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSSGGQIPITTTSSTTTDGSSTPSTPTSTTSASTTTSGGSATTTTGEPITDGSNGGA
SSTTGNSGTTGSATTTTSSSSDNSDGSVGTSTTTSPAITTSSGSIIDPTSPPTTDSSS
NSGGYGSSSSIENGVECLLIITQDAFDSWTYDNIIYTVYQVNLTNIGTLSVESVILTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CelB"
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'db_xref="GI:167881"
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'protein_id="AAA73632.1"
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oin(1196.
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84. .1253
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                                                                                                                                                                                                                                                                                                                                                  45.8%;
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0; Mismatches 186;
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y, NJ 07110-1150, USA
replaced gi:167880.
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                                                                                                                                                                                                                                                                                                                   Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A., Castla,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Devar,K., Depayre,E., Devon,K., Devar,K., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Fuske,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Mellin,J., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Mellin,J., Morris,W., Morrow,J., Mychaleckyj,J., Naula,M., O'Connor,T., O'Donnell,P., Paylin,B., Peterson,K., Pollara,V., Riley,R., Robert,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Torruella-Miller,L., Vassillev,H., Vo,A., Wagner,A., Fireder,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
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AC007435
g5578733
                                            submitted (30-JUL-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1999 this sequence version replaced gi:55237 All repeats were identified using RepeatMasker: Smit, A Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-APR-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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D.rect Submission
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                                                                                                                                                                                                                                                                                          Direct Submission
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Query Match 2.9%; Score 44.4; DB 41; Length 178342; Best Local Similarity 49.2%; Pred. No. 1.5; Matches 117; Conservative 0; Mismatches 121; Indels 0; Gaps	repeat_region compl repeat_region 34981 /rpt_	repeat_region 33888 .33483 /rpt_family="MER45" repeat_region complement(34045" /rpt_family="MER45" /rpt_family="14050.34150)	_region	repeat_region complement(32539.32688) /rpt_family="MEDSA" repeat_region 'complement(32713.33164) /rpt_family="Looper" repeat_region 33251.33339	gion	gion	/rpt_family="Looper" /rpt_family="Looper" /rpt_family="Looper"	repeat_region complement(3074031003) repeat_region complement(3101531082) repeat_region complement(3101531082)	repeat_region	repeat_region 2677726976 /rpt_family="Charliela" repeat_region complement(2700027228) /rpt_family="MIR"	/rpt_ 26485	gion	repeat_region 24619 .24729 /rpt_family="L2" repeat_region 24746 .24823	gion	repeat_region 22511. 22805 /rpt_family="AluJb" reneat_region 22806 22828	repeat_region 20726 .20777 repeat_region 20726 .20777	region	region	repeat_region 18132. 18363 /rpt_family="Alusg" repeat_region 18364. 18389	

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This sequence is co
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5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
For further infomation about this sequence, including its location
and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-NOV-1998) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advance Database Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (F-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens 1,210,381bp genomic DNA of 8p21.3-p22 anti-oncogene hepatocellular colorectal and non-small cell lung cancer region published Only in DataBase (1998) In press 2 (bases 1 to 10000) The colorectal and shimada, J. Yanaguchi, H., Imai, K. and Shimada, J.
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Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
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On Sep 23, 1999 this sequence version replaced gi:4558576.
The Morking draft' sequence. It currently
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tonsists of 16 contigs. The true order of the pieces
to not known and their order in this sequence record is
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Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Paio Alto,
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Best Local Similarity 42.9%;
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                                                                                                                                                                                                                                                                                 TAAATATTTTATGAATATAATATTATTTGATTAATAC 91625
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                                                                                                                                                        complete
AC004106
Muzny,D., Arenson,A.D., Adams,C., Brundage,E., Bunac,C., Carvelli,K., Chacko,J., Chen,J., Di,W., Ding,Y., Dugan,S.
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 190482)
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Homo sapiens Xp22
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              Arenson, A.D.,
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/db_xref="taxon:5833"
/chromosome="12"
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On May 22, 1998 this sequence version replaced gi:3126769.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          were canonical splice junctions across the splice junctions.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exon/Intron boundaries of identified were canonical splice junctions that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The repeat regions shown were identified using RepeatMasker by Adrian Smit \gamma_{ij}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-FEB-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 190482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C., Yu, W., Chinault, C., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simon, M., Stovall, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                       complement (5266)
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complement(2277. .256
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complement/206
                                                                               complement(4760. .4925)
/rpt_family="AluSg/x"
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/rpt_family="AluJb"
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/clone="GSHB-45N23"
                                                                                                                                                                rpt_family-"AluSg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                _family="Alusx"
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complement(5523. .5825

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complement(11189. .11488)
/rpt_family="Alusx"
11712. .12013
                                                                                                                                                                       /standard_name="DXS7171"
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complement(14952..15154)
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                                                                                     /rpt_family="AluSq"
complement(16019. .16320^
/rpt_familv="".
                               complement(17350. .17651)
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                                                                                                                                              complement(15169..15425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="D49677 Human U2AF1-RS2 mRNA, complete cds; Bases
1-143 of cDNA are not found in this clone"
complement(8918. .9217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8185. .8367)
/rpt_family="AluSq"
/rpt_family="AluSq"
join(8601. .8684,12419. .12527,12842. .12898,16964. .17002,
17931. .18049,24408. .24621,27318. .29047,31462. .31988)
/gene="D49677"
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/rpt_family="L2"
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complement(5940. .6
   /rpt_family="AluJo/FRAM"
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/rpt_family="AT_rich"
complement(10888..10908)
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t_family="LIMC4"
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lement(14220
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lement(9960. .10)
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lement(14681. .14799)
_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "AluSp/q"
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                                           SECTENT
SOURCE
ORGANISM
                                                                                                                  ACCESSION
NID
                                                                                                                                                            RESULT 14
ECRHSFEX6
LOCUS
DEFIMITION
                                                                                      VERSION
KEYWORDS
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 REFERENCE
                                                                                                                                                                                                                                                      Db 143506 Trc 143508
                                                                                                                                                                                                                                                                                                                                                                       Eb 143386 FATALTGATCCACTTTATTATAGCTAAAACCTGTCATATCATTACATCTCAAATAACCAA 143445
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Sest Local S
Satches 72
                                                                                                                                                                                                                                                                                1442 ttc .:444
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                 Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                           ECRHSFEX6 2402 bp DNA ECT Escherichia coli extended core protein RhsF partial cds, and unidentified ORF, complete
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7?; Conserv
             Escherichia.
                                                                                                    U15127.1
                                                                          of 6
(bases 1 to 2402)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MTR?
%complement(18965. .19012)
/rpt_family="%2"
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                                                                                                      GI:563992
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complement(20165. .20456)
/rpt_family="(TA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(30101..30540)
/rpt_family="LIM4"
complement(30725...31020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AT_rich"
complement(26719. 26883)
/rpt_family="(CATA)n"
complement(27499. 27802)
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complement/occidents
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complement/corr
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3, .23360
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 11;
Pred. No. 3;
0; Mismatches 50
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and ORF f202 genes,
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Gaps

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Matches 94
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TITLE
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TITLE
JOURNAL
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TATAGATGATATTGGAATATTTGCATTGGCAATGTGTAATGGAGAATCAATTAACGAGAA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-SEP-1994) Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hershey,
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                                                                                       Similarity
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                                                                                                                                                                                 705
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="end of RhsF genetic element and begining
similarity between ECOR-50 and K-12 chromosomes"
complement(1879. .>2402)
                                                                                                                                                                                                                                                                                                                                                                                 complement(1879. .>2402)
/note="identified by similarity to E.
GenBank Accession Number L19201"
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                                                                                                                                                                                                                /translation="ISRSSQSKAIQLATHSDYSHTGMLVMRNKKPYVFEAVGPVKYTP
LKQWIAHGEKGKYVVRRVEGGLSVKQQQKLAQTAKRYLGKPYDFSFSWSDDRQYCSEV
WKYYQNALGMRVGEQQKLKEFDLSSPQVQAKLKERYGKNIPLEETVVSPQAVFDAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSLNFSSKDLTNSYMNGMGKKEYSSYLGTPNNTYLKYNPKAKGNGVTIIRQGSN"
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LKGGWNFYQYPLNPISNIDPLGLYEFKSKNIDDIGIFALAMCNGESINENKEYGGLIC
KKQGEYFPMNPISSNDNDSVDLRNIKCPEGSERVGDYHTHGFYSDDKGNKVTKENDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:562"
1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Escherichia coli"
/insertion_seq="iso-IS1"
/strain="ECOR-50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF downstream of RhsF core with possible signal
peptide for export from cytoplasm"
                                                                                                                                                                                                                                                                        /db_xref-"GI:564001"
                                                                                                                                                                                                                                                                                        /protein_id="AAA66217.
/db_xref="PID:g564001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mkviqccyflalvsshimagvmsddniflsnsdlaalycvakif
/dgeniliykvniinasskkdvffyesptsthndimggggmsyayeydvkynichlrk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="ECOR-50"
/db_xref="taxon:562"
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                                                                                                                                                                                                                                                                                                                               /product="ORF-f202"
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                                                                                                                                                                                                                                                                                                                                             transl_table=11
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db_xref="PID:g563999"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTTCAAATGATAATGATAGTGTAGACTTGCGAAATATAAAATGCCCCTGAAGGTTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JAN-1998) Biochemistry ctate College of Medicine, P.O. Box 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhs elements comprise three subfamilies acquisition by Escherichia coli Bacteriol. 180 (16), 4102-4110 (1998)
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Location/Qualifiers
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                                                                                                                            HYGYDEKGRLIGERQTVHHPQTEALLWQHETRHAYNAQGLANRCIPDSLPAVEWLTYG
SGYLAGMKLGDTPLVEYTRDRLHRETLRRFGRYELTTAYTPAGQLQSQHLNSLLSDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="RhsF accessory genetic element"
| Trpt_family="Rhs accessory genetic element"
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|CDHRGLPLALISTEGATAWCAEYDEWGNLLNEENPHQLQQLIRLPGQQYDEESGLYY
                                                              |RLVHYTRTQYEEPLVESRYLYDPLGRRVAKRVWRRERDLTGWMSLSRKPQVTWYGWD
                                                                                                                                                                                                                                                                                                                                                                                                             ;GHPVNPLLGAKVLPGETDIALPGPLPFILSRTYSSYRTKTPAPVGSLGPGWKMPAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="GI:2920637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="core protein"
'protein_id="AAC32473.1
'db_xref="PID:g2920637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'transl_table=11
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                                                                                                                                                                      TTQGGLTRSMEYDAAGRVIRLTSENGSHTTFRYDVLDRLIQETGFDGRTQRYHHDLT
KLIRSEDEGLVTHWHYDEADRLTHRTVNGETAEQWQYDERGWLTDISHISEGHRVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                    HPDSTLSMWPDNRIARDAHYLYRYDRHGRLTEKTDLIPEGVIRTDDERTHRYHYDSQ
                                                                                                                                                                                                                                                                              ?TYDDKYRGRMVAHRHTGRPEIRYRYDSDGRVTEQLNPAGLSYTYQYEKDHITITDS
DRREVLHTQGEAGLKRVVKKEHADGSVTQSQFDAVGRLKAQTDAAGRTTEYSPDVVT
                                                                                                                                                                                                                                    ONPHSDLPCATDDATGSRKTMTWSRYGQLLSFTDCSGYVTRYDHDRFGQVTAVHRE
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Hershey, PA 17033,
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Best Local Similarity 52.2
Matches 94; Conservative
                                                                                                                                1209 gaatttgggcaaagaatcaagtagtgagtggagtgataaacaatgctgggaaggtgaaga 1268
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/note="similar to insertion element iso-IS1 of Shigella dysenteriae".
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DGENILIYKVNIINASSKKDVFFYESPTSTHNDIMGGGGMSYAYEYDVKYNICHLRK
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OM nucleic nucleic search, using sw model

January 20, 2000, 05:08:09; ; Search time 123.5 Seconds
(without alignments)
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Perfect score: US-09-077-817-1 1539 ggtgcctgtcggcgggaga.....aattttcttgcgaatgttg 1539

Scoring table: Searched: 311585 seqs, 125096042 residues IDENTITY_NUC

Database : N_Geneseq_36:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution

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P-PSDB; W24972.
New purified human interleukin-13 receptors - and related nucleic acids, coeful for diagnosis and treatment of inflammation, allergy, WO9720926-A Caput 07-NOV-1996; F01756. 06-DEC-1995; FR-014424. Interleukin-13 receptor; diagnosis; inflammation; allergy, IL-13; Human inter sukin-13 beta receptor DNA T85826; T85826 standard; DNA; 1539 BP. 72-JUN-1998 SNFI t D, Ferrara P, Laurent P, Vita 97-319773/29.) SPNOFT SA. (first entry) Q28507 T46203 **T4**6204 ALIGNMENTS z Tomato vacuolar in Heliothis virescen Heliothis virescen streptococcus pneu Continuation (11 o Streptococcus pneu

Ď Ş 당 Ş ß δÃ 5#6686868686868686868686868 Query Match Best Local Similarity Macches 1539; Conserv and 427 % proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low affinity; but acquires high affinity when associated with the IL-4 receptor. Nucleic acids encoding IL-13R beta and alpha are used as diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant IL-13R beta and alpha which can be used as IL-13 antagonists, specifically to regulate IL-13-induced responses for treatment of inflammation and of II-13 receptors; when coupled to a toxin also for treatment of averproduction of II-13R. Cells that express II-13R at the surface are used to identify ligands and modulators of III-13R. Note: II-13R beta specification (786464), which is not the same as that shown in the sequence listing (785865) which is not the same as that shown in the sequence 1539 SP: 492 A; 247 C; 335 G; 465 T; This sequence encodes human interleukin-13 (IL-13) beta receptor. The invention relates to new purified peptides comprising 380 or 427 amind acid sequences, which are receptors for interleukin-13 (IL-13); the 38 and 427 as proteins are designated IL-13R beta and alpha respectively allergy. Il-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard immenoassays) to diagnose diseases associated with abnormal expression Claim 6; Fages 41-42; 83pp; French 121 121 ည 61 attogtitgcttggctatoggatgcttatatacottttotgataagcacaacatttggctg 120 1 ggtgcctgtcggcggggagagagggcantatcaaggttttaaatctcggagacatggctta 60 tgagata/jggattatgaagaga.occggatacttaggttatctctatttgcaatggcaa 240 TACAAGC //TTTGCACTTCATCTTCAGACACCGAGATAAAAGTTAACCCTCCTCAGGATTT ATTCGTTTGCTTGGCTATCGGATGCTTATATACCTTTCTGATAAGCACAACATTTGGCTG tacaagcrittgcacttcatcttcagacaccgagataaaagttaaccctcctcaggattt 180 GGTGCCTCTCGGCGGGGAGAGAGGCAATATCAAGGTTTTAAATCTCGGAGAAATGGCTTA 60 Conservative 100.0%; 0: Score 1539;
Pred. No. 0;
0: Mismatches B 0 1; Length 1539; Indels (IL-13); the 380 0 IL-13R beta Gaps 120 0

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GTGCCTGTCGGCGGGGAGAGAGGCAATATCAAGGTTTTAAATCTCGGAGAAATGGCT--
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Conservative

0;

55.7%;

Score 857; DB Pred. No. 4.5e 0; Mismatches

DB 1; ..5e-224;

Length 1298 Indels

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20;

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99t9cct9tc9gc9g9gagagagggcaatatcaaggttttaaatctcggagaaatggctta

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PS Claim 6; Figure 2a: 83pp; French CC This sequence encodes human interleukin-13 (IL-13) beta receptor. The CC invention relates to new purified peptides comprising 380 or 427 amino and 427 am proteins are designated IL-13R beta and alpha respectively. CC The IL-13R beta has high affinity for IL-13R beta and alpha are specified in the receptor. Hucleic acids encoding IL-13R beta and alpha are used as cc such as loss of heterozygosity aberrant synthesis or genetic anomalies. They are also used for production of recombinant IL-13R beta anomalies. CC anomalies. They are also used for production of recombinant IL-13R beta and alpha are used as IL-13 induced responses for treatment of inflammation and cc regulate IL-13. receptors are also useful as antisense molecules for gene cc immunoassays) to diagnose diseases associated with abnormal expression. CC of IL-13 receptors are also useful as antisense molecules for gene cc immunoassays) to diagnose diseases associated with abnormal expression. CC overproduction of IL-13R. Cells that express IL-13R hotomatically to the nucleic acid sequence shown in Figure 2a in the sequence listing (785826).

Sc Sequence 1298 BP; 407 A; 231 C; 266 G; 394 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1997;
07-NOV-1996;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (SNFI ) SANOFI SA.
Caput D. Ferrara P. Laurent
WPI: 97-31973/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                     New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy,
                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; W24972.
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22-JUN-1998 (first entry)
Human interleukin-13 beta receptor I
Interleukin-13 receptor; diagnosis;
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028-FEB-1997; U03124.
R 01-MAR-1996; US-609572.
R 01-MAR-1996; US-609572.
COMMY) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key CDS
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P-PSDB; W35295.

New nucleic acid encoding interleukin-13 receptor binding transformed cells - proteins, antibodies and inhibitors, f treating immunoglobulin E-mediated diseases, e.g. Graves d and in diagnosis.
Claim 1, Pages 32-33; 49pp; English.

The present sequence encodes the human interleukin-13 (IL-13) binding chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a mediator of the known biological activities of IL-13. The present sequence was isolated from human testis library. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to rest igs-mediated conditions, e.g. allergy, asthma and immune complex discriders, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in lammatopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein of the such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the IL-13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding the human IL-13 binding chain of the IL-13 receptor. Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-1 mediator; IL-13 receptor binding inhibition; IgE-mediated condition mediator; as immune complex disorder; ds.
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1369 BP; 436 A; 247 C; 282 G; 404 T;
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18-SEP-1997; U04043.
13-MAR-1996; US-013345.
(ZYMO) ZYMOGENETICS INC.
Baumgartner JW, Farrah TM, New nucleic acid encoding testis-specific cytokine receptor for identification of ligands or antagonists, potentially for male contraceptives or for infertility treatment claim 1; Page 44-46; 79pp; English.

This cDNA sequence encodes a novel ligand-binding receptor, Zc which shares homology with cytokine receptors and is isolated placental polyA+ RNA. The resulting polypeptide is a receptor sytokines (particularly interleukin-13) and is expressed on the 30-MAR-1998 (first entry)
imman Zcytor2 cytokine receptor cDNA.
Cytokine receptor; ligand binding; testi
infertility; antagonist; contraceptive; Homo WPI; 97-470820/43. P-PSDB; W36613. OHara PJ; sapiens. /*tag= a /product= /note= "cy Location/Qualifiers 49. 1191 ,XT ct= ZCytor2 "cytokine" غ Foster ģ testicular cell; tive; diagnostic; spermatogenesis; therapeutic; ds.

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Best Local Similarity
Matches 1284; Conserv
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Sequence 1289 BP; 407 A; 236 C; 258 G; 388 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of testicular cells, probably being involved in spermatogenesis. It comes to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to tree infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions, and as male-specific contraceptives. By blocking the action of II-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in this receptor can also be used to modulate immune function, e.g. in
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HR-1 receptor; cytokine receptor; peptide hormone re
infection; bi.ro; trauma; asthma; allergy; AIDS; apla
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claimed (Claim
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CC This cDNA clone codes for a novel human cytokine/peptide hormone CC receptor, designated HR-1 receptor (see W41502). Plasmid ATG-531, CC comprising HR-1 receptor cDNA contained in vector pBluescript SK+, CC is deposited in E. coli JM101 as ATCC 98069. The clone was collected from a human testis cDNA library. Also claimed are a cc polypeptide comprising amino acids 1-380 or 22-380 of the 380 cc residue HR-1 receptor amino acids sequence, a vector comprising CC protein and polynucleotide, host cells, an agonist to the polypeptide, and an antagonist cc that inhibits the activity of the polypeptide. HR-1 receptor CC diagnosis and (gene) therapy applications, e.g. to increase cc diagnosis and (gene) therapy applications, e.g. to increase cc and to prevent, ameliorate, treat, diagnose and/or burns, CC predisposition to asthma, allergic discorders or disorders of haematopolesis induced by AIDS, aplastic anaemia, congenital or cc cyclic neutropaenia or as a consequence of cytotoxic therapy of sequence 1288 BP; 421 A; 227 C; 252 G; 388 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1271; Conserv
563 agaatggattgcgtatastacaattggcaatatttactctgttcttggaaacctggcata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUN-1996; US-017843.
(HUMA-) HUWAN GENOME SCI INC.
(SMIK ) SWITHKLINE BEECHAM CORP.
Appelbaum ER, Hu J;
98-034974/04.
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84.1%;
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Pred. No. 1e-216;
0; Mismatches 0; Indels 24
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V02295 standard; cDNA; 1288 BP. W02295; V02295; OB-JUN-1998 (first entry) Thomo sapiens cDNA encoding the HR-1 receptor.

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                                                                                                                                                                                                                                                                                                                                                                                                                                      PT DNA encoding human cytokine-peptide hormone receptor - useful for preventing preventing or diagnosing, e.g. lowered resistance to infection, asthma, allergy, or haematopoietic disease Claim 1; Fig 1; 75pp; English.

CC (HR-1 receptor). This, or it's activators or agonists, can be used to CC treat, prevent or diagnose predisposition to lowered resistance to CC infection, asthma, allergic or haematopoietic disorders, e.g. where CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia, neutropaenia or cytotoxic treatments for cancer. Antagonists of the CC conditions associated with overexpression of the HR-1 receptor, e.g. antibodies or fragments of it may be used to treat those listed above. Antibodies may also be used to assay levels of HR-1 receptor, overexpression of which may be diagnostic of tumours, by usual immunoassays; to isolate and identify HR-1 receptor-expressing cells; or CC for affinity purification of the HR-1 receptor. The nucleotide sequence itself may be used to express recombinant HR-1 receptor; as a source of probes for isolating genomic HR-1 clones, PCR primers, diagnostic creagents (particularly to detect gene mutations which may indicate culentification and mapping.

Sequence 1288 BP; 421 A; 227 C; 252 G; 388 T;
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Best Local Similarity
Matches 1271; Conser
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18-DEC-1997.
09-UTL-1996; U11459.
12-UUN-1996; WO-U10262.
12-UUN-1996; U5-017843.
(HUMA-) HUMAN GENOME SCI INC (SMIK ) SMITHKLINE BEECHAM C Appelbaum ER, Hu J;
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WPI; 98-052200 /07
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PT Nucleic acid sequence encoding human cytokine peptide hormone Preceptor - useful to treat, prevent or diagnose, e.g. lowered PT receptor - useful to treat, prevent or diagnose, e.g. lowered PT resistance to infection, asthma, allergy or haematopoietic disease CC claim 4; Page 61-62; 76pp; English.

CC cytokine/peptide hormone receptor, designated the HR-1 receptor cytokine/peptide hormone peptide from a human testis tissue CC production of HR-1 receptor, as a source of probes to isolate CC diagnostic reagent (particularly to detect gene mutations which CC dientification and mapping, and in a claimed method for treating CC and agonists can be used to treat, prevent or diagnose CC and agonists can be used to treat, prevent or diagnose CC or haematopoietic disorders, e.g. where induced by AIDS, aplastic CC anaemia, neutropaenia or cytotoxic treatments for cancer.

SQ Sequence 1288 BP; 421 A; 227 C; 252 G; 388 T;
                                                                                                                                                                                                                                                                        Query Match
Best Local
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P-PSDB; W41520.
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hes 1271;
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(HUMA-) HUMAN GENOME SCI INC.
(SMIK) SMITHKLINE BEECHAM CORP
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disorder; therapy
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12-MAR-1997; U04043.
3 13-MAR-1996; US-013345.
7ZYMO ) ZYMOGENETICS INC.
7ZYMO TOTAL JW, FAIRTAN TM, FY
                                                                                                            Query Match
Best Local Similarity
Matches 1137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding testis-specific cytokine receptor for identification of ligands or antagonists, potentially for male contraceptives or for infertility treatment claim 2; page 49-51; 79pp; English.

This sequence encodes a novel ligand-binding receptor, Zcytor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 2cytor2 cytokine receptor cDNA. Cytokine receptor; ligand binding; testi infertility; antagonist; contraceptive;
                                                                                                                                                                                                                 be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treating intertility. Antagonists of this receptor may be used to characterise ligand receptor interactions and as male specific contraceptives. By blocking the action of II-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor
                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and was isolated from a human testis cDNA library. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can
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                                                                                                                                                                                                                                      New nucleic acid encoding testis-specific cytokine receptor - useful for identification of ligands or antagonists, petentially for use as male contraceptives or for infertility treatment Example 4; Page 53-56; 79pp; English.

This cDNA sequence encodes a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and is isolated from testis tissue obtained from a Celebus macaque. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands promoting proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune cinculating levels of ligand and asto to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as antagonist.

Sequence 1126 BP; 359 A; 191 C; 227 G; 349 T;
                                                                                                                                                               Query Match
Best Local Similarity
Matches 1075; Conserv
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12-SEP-1997; U04043.
13-MAR-1996; US-013345.
(ZYMO ) ZYMOGENETICS INC.
Baumgartner JW, Farrah TM, Foster DC, Grant FJ,
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                                                                                                                                                                 Conservative
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/note= "cytokine receptor"
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Pred. No. 1.2e-160;
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(AMRA-) AMRAD OPERATIONS PTY L1

(Hilton DJ, Nicola NA, Simpson R

WPI; 98-207062/18.

New 1501416-7

prod""
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection
Example 14; Page 50-52; S9pp; English.

The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.

Sequence 1079 BP; 341 A; 209 C; 227 G; 302 T;
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19-MAR-1998.
10-SEP-1997; A
27-FEB-1997; A
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/product= "Mature
/note= "No stop cc
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 595; DB 1;
Pred. No. 9.2e-153;
0; Mismatches 0;
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                                         GCGAAGATACACACGCTTTTACCATGGCAATGC
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WO9810638-A1.
19-MAR-1998.
18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                   1016
                                                                                                                 Key
CDS
                                                                                                                                                                  16-SEP-1998 (first entry)
Mature interleukin-13 binding protein gene.
Therapeutic: IL-3 mediated condition: allergation autoimmune disease; antibody: immunotherapy;
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   AU0591.
                                           /product= '
                                                                                                                                   Location/Qualifiers
                                                     "Mature IL-13 binding o stop codon given""
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allergy;
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Best Local Similarity
Matches 942; Conserv
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10-SEP-1996; AU-002262.
(AMRA-) AMRAD OPERATIONS PTY LT
Hilton DJ, Nicola NA, Simpson R
WPI; 98-207062/18.
P-PSDB; W56261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection
Disclosure; Page 19-20; 69pp; English.
The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
Sequence 947 BP; 312 A; 161 C; 198 G; 276 T;
       872
                              545
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                      tgcgtatattacaattggcaatatttactctgttcttggaaacctggcataggttacatt
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AU-002262.
D OPERATIONS PTY LTD.
No OPERATIONS PTY LTD.
Than Simpson RJ, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.7%; .Score 595; DB 1; Length 947; 82.7%; Pred. No. 8.7e-153; tive 0; Mismatches 0; Indels 1
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Query Match 18.0
Best Local Similarity 85.0
Matches 429; Conservative

18.6%; Score 287; DB 1; 85.6%; Pred. No. 4.8e-69; tive 0; Mismatches (

Indels

72;

Gaps

7;

TO DEF. 144 H; 33 C; 32 G; 129 T;	
So Segmence 456 Bb. 1333. 63 G as Tipe therapy.	
CC cadherin/tumour invasion suppressor activity, tumour inhibition	
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic	
CC activity, tissue growth activity, activin/inhibin activity,	
CC stimulating or suppressing activity happanaronies; regulating	
CC conditions in humans and animals, although no supporting data is	
them suitable for treating, preventing or ameliorating medical	
are predicted to have useful biological activities which would m	
The polynucleatide which is a secreted sem and the accused tag (ESI	
Claim 1; Page 320; 618pp; English	
PT ovary pituitary, retina and colon CDNA libraries.	
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain.	
New polynucleotides encoding human socrated protoing - desired for	
WBT: 00-070077/06	
Agostino MJ, Jacobs K,	
(GEMY) GENETICS INST	
یر ب	
Homo sapiens	
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tu	
growth; activin; inhibin; chemotaxis; chemokinesis	
Human; secreted protein; expressed sequence tag: EST: haematopolesis	
EST Clone C	
V89756;	
789756 standard; cDNA; 456 BP.	
RESULT 12	
TGGAGTGATAAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAACTTTGC	
. 1232	
838 GTAAGAAGCAAAGTGAATATTTATTGCTCAGATGACGGAATTTGG	
)aagcaaagtgaatatttattqctcaqatqacqqaa1	
AATGAAACCC	
aataatagagt	
TTGGTGACTGCTACAGTTGAAAA	
QY: 1052 gatactaccgaaagcatggaggaattttggtgactgctacagttgaaaatgaaacataca 1111	
CONTROL TO THE TOTAL TOT	
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gacctattccagcaaggtgttttgattatgaaattgagatcagac	
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W09810638-A1.

19-MAR-1998.
10-SEP-1997; AU-005374.
110-SEP-1996; AU-005374.
110-SEP-1996; AU-005262.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Hilton DJ, Nicola NA, Simpson RJ, Zhan
WPI; 98-207062/18.
P-PSDB, W56255, W56256, W56257.
New isolated interleukin-13 binding pr
products for therapy e.j. for allergic
for diagnosis or detection
The IL-13 binding protein and related
                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                     Therapeutic; autoimmune di
                                                                                                                                                                                                                                                                         24-SEP-1998 (first entry)
Interleukin-13 binding protein C-terminal region
Therapeutic; IL-3 mediated condition; allergy; as
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                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                     disease; antibody;
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/product-
/note- "No
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/*tag=
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/product= "IL-13
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Collins
Wood C;
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CDS
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                                                         64-SEP-1997, U03124
28-FEP-1997, U03124
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33: W35294.
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) GENETICS INST II
S M, Conaldson D,
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Pred. No. 6.7e
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5.7e-57;
hes 11;
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The present sequence encodes the murine interleukin-13 (IL-13) binding chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a mediator of the known biological activities of FIL-13. The present sequence was isolated from the thymuses of 6.8 week old mice. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in the activity in cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the IL-13 receptor cother than IL-13bc. IL-13bc can also be used in diagnosis to detect expression of IL-13. its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours.

So Sequence 1525 BP; 505 A; .246 C; 327 G; 447 T;
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Best Local Similarity
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                                                                                aggatgcagatttccctatttggcaataaaggagcagtgaggcatcagactataaagatt
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                                                                                                                                                           ATGCCTT-----ACAGTGTGCTGATTACCTCCAGCATGATGAAAAAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACTTGGTTATCTCTATTTGCAATGGAAACCTCCTGTGGTTATAGAAAAATTT-----
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 - proteins, antibodies and inhibitors, for
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63.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ACTATAATTACTAGGAATCTAATTTACAAGGATGGGTTTGATC
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Pred. No. 2.5e
0; Mismatches
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19-MAR-1998.
10-SEP-1997; A
27-FEB-1997; A
                 The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for
                                                                                                                                                                                                                                                                                                                                                                                            SGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1159
                                                                                              New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as astifor diagnosis or detection claim 10; Page 43; 69pp; English.
                                                                                                                                                                  10-SEP-1996; AU-002262.
(AMRA-), AMRAD OPERATIONS PTY LTD.
Hilton DJ. Nicola NA, Simpson RJ,
WPI; 98-207062/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Therapeutic; IL-3 mediated communitherapy; autoimmune disease; antibody; immunotherapy;
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IL-3 mediated condition; allergy; asthma;
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/product= "IL-13 binding protein ORF
/note= "No start codon, stop codons (
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422	362	242 290 302 341	182		62	76	Query Match Best Local & Matches 35%	Sequence
aagata AGGTTA	agaatc AGAATC	ccccac	gagata GAGATA	acaago	ttegtt 	gtgcct GIGCCT	tch al sim 352;	
aagatacacacgctttt AGGTTACACACGGTTTT	jaatctacattac AATCTACATT	tgtctctg	gtggatta GTGGAT	ttttgcac	tgcttggc 	gtcggcgg	14. Query Match Best Local Similarity 80. Matches 352; Conservative	473 BP;
ttt 438 	agaatotacattacaaagatgggtttgatottaacaagggcattgaattatagaagggcg	ccccactgtctctggatcattttgtgttgtgaaaggaatgcacagtggaatatgaactaa	gagatagtggattatgaagagaacccygatacttaggttatctctatttgcaatggcaac 	acaagcttttgcacttcatcttcagacaccgagataaaagttaaccctcctcaggatttt	THEOGRAPHICACATAGE TO THE TRANSPORT OF T	gtgcctgtcggcggggagagaggcaatatcaaggttttaaatctcggagaaatggcttaa 	14.4%; 80.5%; ative	134 A;
	gtttgatci ATGGGGTT	tgtgttgttg AACATGGGJ	acccygata -CCCGGATA	cagacacco	gcttatata CTTATATA	gcaatato: CAATATC!	Score Pred. 0; Mi	92
	ttaacaag GGATCNT	yaaaggaa AAGGAA aggctagt AAG	acttaggt ACTTAGGT	gagataaa SAGATAAA	acctttct	aaggttt NAGGTTTT	Score 221.6; DB 1; Pred. No. 3.1e-51; Mismatches 35;	C; 11
	ggcattg TAACAAG	tgcacag	tatetet TATETET	lagttaac	gataago	aaatctc AAATCTC	DB 1; 35;	114 G;
	aattata GGGCATT	rtggaata	atttgca ATTTGCA	CCTCCTC	acaacat ACAACAT	ggagaaa: GGAGAAA	Length dindels	131 T;
·	gaagggc GAAGGCG	rgaacta GAACTA CATTACT	atggcaa ATGGCAA	aggattt	ttggctg	tggctta GGCT	473; 50;	
	g 421 A 445	a 301 	c 241 C 289		t 121 192	a 61 - 133	Gaps	
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Search completed: January 20, 2000, 06:16:48 Job time: 4119 sec



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Title:
Perfect score:
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Copyright (c) 1993 - 1998 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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126;

Gaps

10;

860

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Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL
                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg,
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Unpublished (1997
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                      E Consortium (info@image.llnl.gov) for primer: -40UP from Gibco
                                                                                                                                                                                                                                                         quality sequence stop: 468
       /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung mbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driv was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2348766"
/clone_lib="soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                             1341 atatitgtaaccggictgcitagtgaatgtigcgtaagccaaacaccitacccaaaaatga
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                                                                                                                                 atttttettgegaatgttg
                                                                                                                                                                               gtattgactcaacaĝtttccagtcatggccaaatgttcaatatgagtctcaataaactga
                                                                                                                                                             GTATTGACTCAACAGTTTCCAGTCATGGCCAAATGTTCAATATGAGTCTCAATAAACTGA
                                                                                                                                                                                                                         TTCCAGAATTTTTCTGTGATACATGAAGA----
                                                                                                               ATTTTTATAACGAATGTTG
                                                                                                                                                                                                                                     ttccagaatttttctgtgatacatgaagaagatttgcatctttccatatccagagacatg
                                                                                                                                                                                                                                                                                                                                                   aactttgctagttagctgggatcgtttctggctaccatttggtttcatcttaatattagtt 1340
                                                                                                                                                                                                                                                                                    ATATTTGTAACCGGTCTGCTT-----
                                                                                                                                                                                                                                                                                                                                                                                                          agaatcaagtagtgagtggagtgataaacaatgctgggaaggtgaagacctatcgaagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcagagaagatgatactaccgaaagcatggaggaattttggtgactgctaccagttgaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ATCAGATCCAGTTATTTCACTTGTCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAG
 AI358911 479 bp mRNA EST 15-FEB-1999 qy19c05.x1.NCI_CGAP_ETN23 Homo sapiens cDNA clone IMAGE:2012456 similar to SW:II32_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR ; mRNA sequence.
                                              AI358911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTATAGAGATATCTATATTTGTGTAAATGGATCATCAGAGAACGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctataaagatttctatatttgtgttaatggatcatcagagaacaagcctgaaatatcaag
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                                                                                                                                                                                                                                                                                                                                                                                        -AGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGAAAACCTATCGAAGAA
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Soares and M. Fatima Bonaldo. "
a . 133 c 117 g 221 t
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82.68;
tive *
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mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  -CGTTTCTGGCTACCATTTGGTTTCATCTTAATATTAGTT
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Pred. No. 3.5e-92;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TTGGTGACTGCTACAGTTGAAAA
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JOURNAL COMMENT

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               1025 gattatgaaattgagatcagagaagatgatactaccgaaagcatggaggaatttttggtga 1084
                                                                                                                                                                                                      479 ATTAAGCTGAAATGGAGCATACTTT---
                                                                                                                                                                                                                        965 attaagctgaaatggagcatacctttgtttaggcgtggacctattccagcaaggtgtttt 1024
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                        GATTATGANATTGAGATCAGAGAAGATGATACTACC------
                                                                     CTGCTACAGTTGAAAATGGAACATACGCCTTGAAAACAACAAATGAAACCCGA-----
                                                                                                                                                                                                                                                                           468;
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94110532
AI358911.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Discorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: Greg Lennon,
                                                                                                                                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2012456"
/clone_11b="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                         19.7%;
                                                                                                                                                                                                                                                                       Score 303; DB Pred. No. 1.2e 0; Mismatches
                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                      DB 45;
l.2e-62;
nes 11;
                                                                                                                                                                                                      TGGGCCCTATCCAGCAAGGTGTTTT 430
                                                                                                                                                                                                                                                                                                                                                                                                            the modified pT7T3 vector. constructed by Bento
                                                                                                                                                                                                                                                                                                       Length 479;
                                                                                                                                                                                                                                                                                                                                                                              1 others
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 GACGGAATTTGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 ACCTACCCAAAAATGATTCCAGAATTTTTCTGTGATACATGAAGA-----CTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LINL; contact the IMAGE Consortium (information.lnl.gov) for further information. Insert Length: 609 Std Exror: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 19, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/note="Organ: pooled; Vector: pT/T3D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.ncbi.nlm.nih.gov/ncicgap.
Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1523637"
/clone_1lb="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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nes 439; Conservative
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         Contact: Wilson RK
Washington University Sche
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 360)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost, Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

Unpublished (1997)
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est@watson.wustl.edu
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Best Local Similarity 88.4%;
OPGANISM '
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                                                                                                        yg99f10.s1 Soares
IMAGE:41648.3', mF
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R52796.1 GI:814698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "68 c 61 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratories, Inc., and primed with a Not I - oligo(dT) orimer (5')
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55 Std Error: 0.00
                                                                                                                             infant brain
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                                                                                                                                                                                            acggaatttgggcaaagaatcaagtagtgagtggatgataaacaatgctgggaaggtga 1265
                                        atcttaatattagttatatttgtaaccggtctgcttagtgaatgttgcgtaagccaaaca
                                                                                                                                                                       ACGGAATTTGG------AGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGA
                                                                                                                                                                                                                                                                                                                                                 CTACAGTTGAAAATGAAACATACACCCTTGAAAAACAACAAATGAAACCCGACAATTATGC 346
                                                                                      AGACCTATCGAAGAAAACTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                          381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stops: 382 Source: IMAGE Consortium, This clone is available royalty-free through LLNL; contact IMAGE Consortium (info@image.llnl.gov) for further informationsert Length: 1454 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 1454
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2 79 g 158 t 1 others
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ACTGGAAGAATTCTTTTTTTTTTTTTTTTTT 3'];
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/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
l; Site_2: Hind III; 1st strand cDNA was primed with a No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
/db_xref="GDB:414189"
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                                                                                   -------CTACGTTTCTGGCTACCATTTGGTTTC
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Pred. No. 3.8e-48;
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Email: Robert fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ws05c01.x1 NCI_CGAP_Xid11 Homo sapiens cDNA clt similar to SW:I132_HUMAN Q14627 INTERLEUXIN-13 CHAIN PRECURSOR ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    seq primer: -40UP from Gibco
High quality sequence stop:
Location/Qualifiers
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cione distribution: NCI-CGAF clone distribution cup through the I.M.A.G.F. Consortium/LLNL at:
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                    136
            /note-"Organ: kidney; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: No: I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "3 145 t 5 others
                                                                                                                                                                                                                               /clone="IMAGE:2496283"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                 'organism="Homo sapiens"
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Best Local Similarity 88. Matches 333; Conservative

15.5%;

Score 239; DB 63; Pred. No. 2.5e-47; Mismatches

Length 446;

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Query Match

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REFERENCE
AUTHORS
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ORGANISM
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Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1454
High quality sequence stops: 372 Source: IMAGE Consortium, LLNI
This clone is available royalty-free through LLNI, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1454
Std Error: 0.00
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                                                                                                                                                                                                                                      Washington University Scho 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                       Contact: Wilson RK
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IMAGE:41648
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/organism="Homo sapiens"
/db_xref="GDB:414189"
/db_xref="taxon:9606"
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8 5', mRNA sequence.
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RESULT R52795

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Earle-Hughes, J.,

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422 aagatacacacgctttt 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 gagatágtggattatgaagagaacccggatacttaggttatctctatttgcaatggcaac
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                 White, C., Sutton, G., Blake, J.A., Brown, Brown, Brown, G., Blake, J.A., Brown, G., Blake, G., Blake,
                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertek
Eutheria; Primates; Catarrhini; Hominidae; Hon
1 (bases 1 to 355)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                               AA298563 365 bp mRNA EST114178 HSC172 cells I Homo sapiens receptor (IL13R), mRNA sequence,
                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                        GI:1950896
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Pred. No. 3.7e-43;
0; Mismatches 35
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Weinstock, K.G., Gocay
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                                                                                                                                                                        Vertebrata;
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                                                                      Fuldner, R.A.,
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                                   Gocayne, J.D.,
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ORIGIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATTGGATATCACCACAAGGAATTCCAGAAACTAAAGTTCAGGAT------
                         agatttctatatttgtgf,taatggatcatcagagaacaagcctgaaatatcaaggaatca
|||||||||||
                                                                                                                                                                                                                  ggatcatgcattaaatatatttggaaacagtgtgttgattacatcaaggctgatggacaa
  AGATTTCTATATTTGTGTTAATGGATCATCAGAGANCAAGCCT
                                                                                                                                       aatataggatgcagatttccctatttggcaataaaggagcagtgaggcatcagactataa
                                                                                            AATATAGGATGCAGATTTCCCTATTTG------GAGGCATCAGACTATAA
                                                                                                                                                                                                                                                                                                                                                                                   TGGATTGCGTATATTACAATTGGCAATATTTACTCTGTTCTTGGAAACCTGGCATAGGT- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature, 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96026280
On Sep 12, 1996 this sequence version replaced g1:1393411.
Other_ESTs: THC194124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
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Glodek, A., Gnehm, C.L., Hanna, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute for Genomic Medical Center Drive,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="HSC172 cells I"
/cell_type="fibroblast"
/cell_line="HSC172 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-;
ECORI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="ATCC (inhost):178283"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
                                                                                                                                                                                            -ACAGTGTGTTGATTACATCAAGGCTGATGGACAA
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117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3132 row: D column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seat
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SADJEAS genomic clone Plate=3132 Col=9 Row=D, genomic survey
CNSC039G
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Location/Qualifiers
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Class: BAC ends
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Fax: (206) 616-3887
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Futheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                 794
                                                                                                                                856 tcaaggaatcagatccagttatttcacttttcagcttcaaaatatagttaaacctttgcc 915
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, PiecoRI digestion of Drosophila Dro
                                                                                 KRDAADDRDDAATWTTWTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDDRDRAGTAGR
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Similarity 15.6%; Pr
86; Conservative 253;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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fly) genomic survey sequence.
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/db_xref="taxon:7227"
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Pred. No. 0.00074;
33; Mismatches 210;
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975 aatggagcatacctttgtttaggcgtggacctattccagcaaggtgttttgattatgaaa 1034
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP). Ittp://www.edgp.ebi.ac.uk. - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota;
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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BACN15A12 of DrosBAC library from Drosophila melanogaster
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/plasmid="pBeloBACII"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15A12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
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                                    /lab_host="DHIOB" (Life Technologies)"
/note="Vector: p773D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EOR; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos, after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries
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1 to 160)
                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/clone_lib="UI-R-C3"
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source

/clone_lib="DrosBAC" /clone="BACN15K18" /note="end : T7" a 171 c 199 g

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197

/organism="Drosophila /plasmid="pBeloBAC11" /db_xref="taxon:7227"

melanogaster"

pBeloBAC11

Location/Qualifiers

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Query Match
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f1
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton oroject grant. The DNA was prepared from embryos by Alain Bucheton
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1 (bases 1 to 1101)
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                                                                                                                  /clone_lib="DrosBAC"
/clone="BACN37D10"
/note="end : SP6"
a 268 c 128 g
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/plasmid="pBeloBAC11"
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                                                                                                                                                                                                                                                                Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The Bogb is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 around constructed by partial EcoRI digestion of Drosophila and provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
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Etaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
                                                                                                                                                                          and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can l found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                        /clone="BACR05D19"
/note="end : T7"
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Query Match

2.9%;

Score 44.8;

DB 69;

Length 1101;

용 Ş 밁 ş 밁 Ş 밁 Best Local Similarity 31.0%; Pred. No. 0.87; Matches 91; Conservative 81; Mismatches 117; Indels 1138 ataatagagtttttagtagcaattatgcttt-----gtagtaagaagcaaagtgaatatt 1192 1;

Search completed: January 20, 2000, 05:25:26 Job time: 6339 sec

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OM protein - protein search, using sw model

Run on:

January 19, 2000, 20:00:50 ; Search time 34.07 Seconds (without alignments) 296.858 Million cell updates/sec

US-09-077-817-4 2324 1 MEWPARLCGTERRY

Perfect score:

Sequence: MEWPARLCGLWALLLCAGGG......QTKEETDSVVLIENLKKASQ 427

Scoring table: BLOSUM62

Searched:

188963 segs, 23686106 residues

Database : A_Geneseq_36:*

Word size :

Number of hits that pass the threshold

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

밁 Ç

241 DDLYVQWENPQNFISRCLFYEVEVNNSOTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300

QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVK9DPPHIKNLSFHN 240 QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN 240

181

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	W59804	щ	425	4 7.5	E.	45	
Novel haemopoietin	425 1 W55012	۳	425	175 7.5	17!	44	
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Overy Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of IL-13 receptors: when coupled to a toxin also for treatment of overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R. Sequence 427 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fages 46-47; 83pp: French
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New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SNFI ) SANOFI SA.
Caput D, Ferrara P, Laurent P, Vita N;
WPI; 97-319773/29.
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Human interleukin-13 alpha
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                                                                121
                                                                                                                                                                        "1 MCSLWYFSHFGDKQDKKIAPETRASIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP 120
                                                                                                                                                                                                                                                                      MEMPARICGIWALLICAGGGGGGGGGAAPTETQPPVTNLSVSVENICTVIWTWNPPEGASS 60
                                                                                                                                                                                                                                                                                                             \ZY\carlcGlwalli.cagGGGGGGAAPTETQPPVTNLSVS\T\TCTVIWTWNPPEGASS 60
                                                                PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG 180
PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG 180
                                                                                                                                    NCSLWYFSHFGDKOUKKIAPETRRSIEVPLNERICLQVGSQC::TNESEKPSILVEKCISP 120
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100.0%; 27; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha receptor.
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Pred. No. 9.7e-211;
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23-OCT-1996; AU0668.
23-OCT-1995; AU-006135.
22-DEC-1995; AU-007276.
09-SEP-1996; AU-002208.
                                                                                                               DNA encoding animal haemopoietin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated by IgE production

Claim 5; Page 52-54; 93pp; English.

Novel mouse and human haemoprotein receptors (W09821 and W09822),

designated NR4, comprise the interleukin-13 (IL-13) receptor

alpha-chain. The human NR4 amino acid sequence was deduced from a composite DNA sequence (T66165) derived from bone marrow cDNA clones. Recombinant NR4, or fusion proteins including NR4, can be produced in transformed host cells. The receptor molecules and their components are useful in the development of a range of
                   agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor, esp. for the development of cpds. capable of modulating the activity of IL-13 and related cytokines such as interleukin-4 for the treatment of allergy, asthma
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T66165.
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W09822;
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    other conditions relating to IgE.
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/label= Transmembrane_domain
367..426
/label= Cyton'-
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/note* "Ig-like domain"
36
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Bust Local Similarity 99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse interleukin-12 receptor alpha chain NR4 NR4; haemoprotein receptor; interleukin-13 recytokine; allergy; asthma; therapy.
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                                                                                                                                                                                                                                                                                                                   .104
                                                                                                                      343. .366
/note= "unidentified
                                                                                                                                                                                                                                                                 /label= N-glycosylation_site
119...342
                                                                                                                                                                                                                                                                                                                                                                              /label= Extracellular domain
/note= "Ig-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                     28...118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                            /label= Cytoplasmic_tail
                                                                                                                                                                                                                                      /label= Haemoreceptor_receptor-domain
                                                                                                                                                                                                                                                                                                                                    'label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Mat_protein
                                                                                                                                                                                       'label N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label Sig_peptide
                                                                                                                                          label= WSDWS_motif
                                                                                           label- Transmembrane_domain
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Pred. No. 2.3e-209;
0; Mismatches 0;
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amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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23-OCT-1995; AU-006115.
22-DEC-1995; AU-007276.
09-SEP-1996; AU-007208.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Hilton DJ, Metcalf D, Nicola NA,
W58987 standard;
W58987;
11-SEP-1998 (fi
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les 319; Conservative
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                                                                                                                                                                          IVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE 420
                                                                                                                                                                                                                                   GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
                                                                                                                                                                                                                                                                                             DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
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                            Protein; 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1708.5; DB 1; Pred. No. 8.9e-153; 0; Mismatches 66;
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Mest Local S
Matches 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          emeliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers for tissues, molecular weight markers for gels, primers or probes, for nutrition as carbon, nitrogen or carbohydrate source. They can also be used as a cytokine for cell proliferation and differentiation activity, as immune stimulants or suppressors, e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding novel secreted proteins—usefulanti-inflammatory, immuno-stimulatory or suppressing at Disclosure; Page 81-82; 110pp; English.

The sequence is that of a secreted protein encoded by an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or
                                                                                                             (TAKA/) "AKATSU K. Takatsu K, Tominaga A, Takagi S, WPI; 92-990329/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-inflammatory or Sequence 177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic lupus erythematosus, to regulate haematopoiesis, for tissue growth, as an activator or inhibitor, or as a chemotactic or chemokinetic, haemostatic and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitor agents.
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Agostino MJ, Jacobs K,
Racie LA Spaulding V,
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Home sapien:
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                                             involving IL-5
Claim 7: Page 21-23;
                                                                                                                                                       11-SEP-1991; 508309.
11-SEP-1990; JP-240638.
                                                                                                                                                                                                                                                                    R22211;
22-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1998.
                                                                                                                                                                                                                                     Autoimmune disorder;
                                                                                                                                                                                                                                                     Sequence of
                                                                                                                                                                                                                                                                                                   R22211 standard; Protein; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-1996; US-726237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                              for treatment of auto-immune
                                                                                                Human and murine
                                                                                                                                                                                                         EP-475746-A.
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The inventors claim: an is
(secretcry) interleukin-5
murine early, B cellomRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 MYKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYYQWENPQNFISRCLFYEVEV 264
                                                                                                                                                                                         8-MAR-1992
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                                                                                                                                                                                                                                                                    (first_entry)
                                                                                              interleukin-5
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                                                                                                                                                                                                                                     therapy;
                                                65pp; English
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Treacy M;
 isolated cDNA sequence encoding murine
-5 (IL-5) receptor, which is synthesised
A; an isolated murine (secretory) IL-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 942; DB 1;
Pred. No. 3.7e-81;
                                                                              -5 receptor and DNA encoding and eosinophilia conditions
                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                     -5) receptor with signal peptide.
eosinophilia.
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                                                                                                                             Murata
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Matches 97
            The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (II-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) II-5 receptor; an isolated cDNA sequence encoding human (secretory) II-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) II-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; an isolated cDNA sequence encoding human (secretory) II-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) II-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human II-5 lacking a cytoplasmic and a transmembrane region; and an expression vector.
                                                                                                                                        Disclosure; Page 45; 65pp; English.
                                                                                                                                                                                                                                Takatsu K,
WPI; 92-09
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-1992 (first entry)
Sequence of interleukin 5 receptor (IL-5R.8).
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      Autoimmune disorder; therapy;
                                                                                                                                                         involving IL-5
                                                                                                                                                                         Human and murine interleukin-5 for treatment of auto-immune au
                                                                                                                                                                                                              7-PSDB; Q22976
                                                                                                                                                                                                                                                                 (TAKA/) TAKATSU K.
                                                                                                                                                                                                                                                                               18-MAR-1992.
11-SEP-1991; 308309
11-SEP-1990; JP-240
                                                                                                                                                                                                                                                                                                                                    EP-475746-A.
                                                                                                                                                                                                                                                                                                                                                                       peptide
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                                                                                                                                                                                                                            tsu K, Tominaga A, Takagi S, Murata
92-090329/12.
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97; Conserv
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No. 7.
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7.5e-22;
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                                                                                               Claim 8; Page 24-25; 65pp; English.

The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (II-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) II-5 receptor; an isolated cDNA sequence encoding human (secretory) II-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) II-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human II-5 lacking a cytoplasmic and a
                                                                                                                                                                                                                                                                           Human and murine interleukin-5 receptor and DNA encoding for treatment of auto-immune and eosinophilia conditions
                                                                                                                                                                                                                                                                                                            Takatsu K, Tominaga A, Takagi S, WPI: 92-090329/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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11-SEP-1990;
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Sequence of interleukin
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                                                                                                                                                                                                                                                             nvolving IL-5
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                                                                      398 AA;
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                                                                                      region; and an expression vector
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.5e-22
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Matches Query Match Eest Local

l Similarity 97; Conser

Conservative

74;

Mismatches

179;

Gaps 90

Score 318; DB 1 Pred. No. 7e-22;

DB 1;

33 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHF-GDKQDKKIAPETRRSIEVPL

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which shares nomology with cytonine acception. The resulting polypeptide testis tissue obtained from a Celebus macaque. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands promoting proliferation spermatogenesis. It can be used to detect ligands promoting proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1998 (first entry)
Celebus macaque Zcytor2 protein.
Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
Infertility; antagonist; contraceptive; diagnostic; therapeutic.
                                                                                                      and/or differentiation of such cells in cultures and may also be used treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding testis-specific cytokine receptor for identification of ligands or antagonists, potentially for male contraceptives or for infertility treatment
                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and is isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OHara PJ;
WPI; 97-470820/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baumgartner JW, Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1997.
12-MAR-1997; U04043.
13-MAR-1996; US-013345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W36616 standard; Protein;
express the receptor, Sequence 372 AA;
                                                   Antibodies can be used to assay circulating receptor (an abnormal may be indicative of disease such as cancer), for labelling cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 56-57; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T96784
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ERICLOV----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---

ESKCVTIL::KGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN

Q

33 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91

Query Match Matches

102;

Similarity

12.8%; ilarity 24.8%; Conservative (

65;

180;

Indels Length

65;

Gaps

16;

Score 296.5; DE Pred. No. 8.1e-2 55; Mismatches 1

BB 1; --20;

5

PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY

-QVKINAPK-EDDYETRIT

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                                                                                                                                                                                                                                                encoding it, for treatment of interleukin-5 mediated disorders such as chronic asthma claim 7; Fig 1; 15pp; English.

This amino acid sequence was deduced from the nucleotide sequence, isoluted as detailed in Q25790. The cytoplasmic domain is 58 mmino acid sequence in signal transduction processes cun not be found in this short cytoplasmic tail. Recombinant IL-5 alpha chain can be used as an IL-5 antagonist in chronic asthma or other disease states with demonstrated esosinophilia. It may also be used either alone or with the beta chain of the whole IL-5 receptor as a tool for screening for IL-5 antagonists. See also Q25790-2,R25063.
                                                                                                                                                                                                             (HOFF) HOMEMANN LA ROCHE'S Devos R, Fiers W, Plaetinck WFI; 92-218502/27.
                                                                                                                                                                                                                                                                                                                                                                   Interleukiu-5; chronic ast
Sequence
                                                                                                                                                                                                                                                                                                                                                 screenin, antagonists;
                                                                                                                                                                 Recombinant alpha chain of human interleukin-5 receptor - and encoding it, for treatment of interleukin-5 mediated disorders
                                                                                                                                                                                                N-PSDE; Q25790
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 WNPPEGASS--NCSLWYFSHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WSEWSDKQCWEVEFLLKKTL---LLFLLPF---GFILILVIFVTGL
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for screening for IL-5
421 AA;
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Pred. No. 2e-20;
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Sequence

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Claim 11; Pages 34-35; 49pp; English.

The present sequence represents the human interleukin-13 (II-13) binding chain of the interleukin-13 receptor, designated II-13bc. II-13bc acts a mediator of the known biological activities of II-13. Recombinant II-13bc proteins, and antibodies raised against them, are used to inhibit the binding of II-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex to treat IgE-mediated conditions, e.g. allergy, asthma and Grave's disease. They are also used to treat immune deficiency (particularly in hematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate II-13 activity, a protein with such activity is combined with II-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the II-13 receptor other than II-13bc. II-13bc can also be used in diagnosis to detect expression of II-13, its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W35295;
27-MAR-1998 (first entry)
Human IL-13 binding chain of the IL-13 receptor.
Interleukin-13; IL-13; interleukin-13 receptor b
Interleukin-13; IT-13; receptor binding inhibition; Igf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W35295
W35295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood C;
war: 97-448632/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1996; US-609572.
(GEMY) GENETICS INST II
Collins M, Donaldson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding interleukin-13 receptor binding chain transformed cells - proteins, antibodies and inhibitors, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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/note= "putative"
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                                          New nucleic acid encoding testis-specific cytokine receptor - useful for identification of ligands or antagonists, potentially for use as male contraceptives or for infertility treatment claim 2; Page 47-48; 79pp; English.

This sequence represents a novel ligand-binding receptor, 2cytor2, which shares homology with cytokine receptors and was isolated from placental polyA+ RNA. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surf of testicular cells, probably being involved in spermatogenesis. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Zcytor2 cytokine receptor protein. Cytokine receptor; ligand Minding; testi
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W36613;
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                               be used to detect ligands that promote proliferation and/or
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                                                                                                                                                                                                                                       Baumgartner JW,
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13-MAR-1996; US-013345
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Best Local S
Matches 107
                                                                                       17-DEC-1997.
04-JUN-1997; 303815.
12-JUN-1996; US-017843.
(HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
APPELDAUM ER, Hu J;
   Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used tassay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor,
                                                                                                                                                                                                                                                                                                                         Human cytokine/peptide receptor, HR-1 receptor.
HR-1 receptor; cytokine receptor; peptide hormone receptor;
Infection; burn; trauma; asthma; allergy; AIDS; aplastic and
                                                               WPI; 98-034974/04.
N-PSDB; V04075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERNVENTS---CEMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM-----SIGKK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTATVENETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV
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                                  cytokine/peptide
ase resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
107; Conser
   Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                therapy
   27-28;
                                                                                                                                                                                                    /label- Mat_protein
/note- "Claim 14"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                   /label= Sig_peptide
                                                                                                                                                                                                                                    .380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%;
34pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GFILILVIEVTGL--LLRKPNTYP-KMIPEFFCD
                                hormone receptor, HR-1 receptor - useful to infections in individuals with trauma and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----RSKVNIYC-SDDGIWSEWSDKQCWEGEDLSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 295.5; DB:
Pred. No. 8.6e-20;
3; Mismatches 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
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                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This protein comprises a novel human cytokine/peptide hormone creceptor, designated HR-1 receptor. The amino acid sequence was dediced ifrom a cDNA clone (see V04075) isolated from a human contestis cDNA ilbrary. It shows 27% amino acid identity and 52% similarity with the human interleukin-5 receptor. Also claimed are polypuclectides encoding HR-1 receptor, vector and host cells, an agonist to the polypeptide, antibody against the polypeptide, and contesting a disease, or a susceptibility to disease, related to expression of HR-1 receptor, and a method for identifying compounds that activate or inhibit the HR-1 receptor. HR-1 receptor protein and polynucleotides can be used for research, biological, diagnosis and (gene) therapy applications, e.g. to increase resistance to infections in individuals with trauma and/or burns, and to prevent, ameliorate, treat, diagnose and/or determine predisposition to asthma, allergic disorders or disorders of cyclic neutropaenia or as a consequence of cytotoxic therapy of cancer, 19mphoma, leukaemia and/or bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Eest Local Similarity
Natches 107; Conserv
(8-DEC-1997.
09-JUL-1996;
12-JUN-1996;
                                                                                                                                                                                   syndrome;
                                                                                                                                                                                                                             w33603;
08-JUN-1998 (first entry)
                                                     109747742-A1
                                                                                                                                                                                                    Cytokine: hormone receptor; AIDS; acquired immune
                                                                                      reptide
                                                                                                           Key
                                                                                                                                              asthma; allergic; haematopoietic;
                                                                                                                                                                 infection
                                                                                                                                                                                                                       Homo sapiens HR-1 receptor.
                                                                                                                                                                                                                                                                             W33603
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                                                                                                                           Home sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYTELISTIFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEY- 70
                                                                                                                                                                                                                                                                                                                                                                        TLLRFWLPF - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIKNLSFHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERNVENTS---CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM-----SIGKK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVDYIKADGONIGCREPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- VYLTFTRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTT-----LVTATVENETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ
                                                                                                                                                                                                                                                                             standard; Protein;
                                                                                                                                                            aplastic anaemia; neutropacnia; cancer treatment; resistance; diagnosis; tumours; HR-1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 AA;
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U11459.
WC-U10262.
                                                                                                         Location/Qualifiers
                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
26.0%;
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                                                                     "signal peptide'
                                                                                                                                                                                                                                                                             380
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RESULT 14
W24972
ID W24972
AC W24972
AC W24972
DT 22-JUN
DE Human
KW Interl
OS Homo s
PN W09720
PD 12-JUN
PF 07-NOV
PR 06-DEC
PA (Surl
PI Caput
Lagran
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Best Local S
Matches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prinfection, asthma, allergy, or haematopoletic disease
Claim 15; Fig 1; 75pp; English.
CC The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or it's activators or agonists, can be used to
CT treat, prevent or diagnose predisposition to lowered resistance to
CT infection, asthma, allergic or haematopoletic disorders, e.g. where
CT induced by acquired immune defliciency syndrome (AIDS), aplastic anaemia,
CT receptor, e.g. antibodies or fragments of it may be used to treat
CT conditions associated with overexpression of the HR-1 receptor, e.g.
CT those listed above. Antibodies may also be used to assay levels of HR-1
CT receptor, overexpression of which may be diagnostic of tumours, by usual
CT infuncoassays; to isolate and identify HR-1 receptor-expressing cells; or
Sequence 380 AA;
12-JUN-1997.
07-NOV-1996; F01756.
06-DEC-1995; FR-014424.
(SNFI ) SANOFI SA.
Caput D, Ferrara P, Laurent P
WPI; 97-319773/29.
                                                                                                                      22-JUN-1998 (first entry)
Human interleukin-13 beta receptor.
Interleukin-13 receptor; diagnosis;
                                                                                                Homo sapiens.
WO9720926-A1.
                                                                                                                                                                                       W24972 standard; protein; 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-1996; US-017843.
(HUMAN) HUMAN GENOME SCI IN
(SMIK) SMITHKLINE BEECHAM
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107; Conser
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N GENOME SCI INC
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Pred. No. 8.6e-20;
Mismatches 169;
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              Vita
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                                                                                                                      inflammation;
                                                                                                                      allergy;
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RESULT 15
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ID W41520
AC W41520
DT 22-JUN
DE Human 1
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FH Key
FT Peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC invention relates to new purified peptides comprising 380 or 427 amino CC and 427 am proteins are designated II-13R beta and alpha respectively. CC The II-13R beta has high affinity for III-13R beta and alpha has low CC affinity, but acquires high affinity when associated with the II-4 CC diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal CC anomalies. They are also used for production of recombinant II-13R beta and alpha which can be used as II-13 antagonists, specifically to CC allergy. II-13 receptors are also useful as antisense molecules for gene CC allergy in the sign of II-13R). Antibodies are used (in standard CC immunoassays) to diagnose diseases associated with abnormal expression overproduction of II-13R coupled to a toxin also for treatment of used to identify ligands and modulators of II-13R. Note: II-13R beta CC used to identify ligands and modulators of II-13R. Note: II-13R beta CC specification (T86464), which is not the same as that shown in the CC sequence listing (T85828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Bert Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                              Human HR-1 receptor:
HR-1 receptor; human; cytokine; infection; haematopoietic disorder; tumour; therapy;
      Peptide
                                 Homo sapiens.
                                                                                                                     22-JUN-1998 (first entry)
                                                                                                                                                               W41520 standard; Protein;
                                                                                                                                                    W41520
                                                                                                                                                                                                                                                                         340 TLLREWLPE-----
                                                                                                                                                                                                                                                                                                 340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 HIKNLSFHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Figure 2a; 83pp; French
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                                                                                                                                                                                                                                                                                                                                                        TLKTTNETRQLCFVV
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                                                                                                                                                                                                                                                                                                                                                                                                                           --VYLTETRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTT----LVTATVENETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-ENIFREGOYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSDDTNYTLYYWHRSLEKIHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA
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Location/Qualifiers
1. .21
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                                                                                                                                                                                                                                                              -GFILILVIFVTGL--LLRKPNTYP-KMIPEFFCD
                                                                                                                                                                   380
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Pred. No. 8.6e-20;
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                                                     therapy; diagnosis
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                                                                      asthma; allergy;
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rising 380 or 4
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PT Protein 22.380

FT W99747741-Al.

/label- Mat_protein
PN W9747741-Al.

/label- Mat_protein
PN W9747741-Al.

/label- Mat_protein
PN 18-DEC-1997.

PF 12-JUN-1996; U10262.
PR (SMIK ) SWITHKLINE BEECHAM CORP.
PA (HUMA-) HUWAN GENOME SCI INC.
PA (SMIK ) SWITHKLINE BEECHAM CORP.
PI Appelbaum ER, Hu J;
PR WF1; 98-052308/05.

PR N-SSDB; V04131.

PR Nucleic acid sequence encoding human cytokine peptide hormone receptor useful to treat, prevent or diagnose, e.g. lowered pr resistance to infection, asthma, allergy or haematopoietic disease Claim 13; Page 62-64; 76pp; English.

CC This protein comprises a novel human cytokine/peptide hormone receptor, designated the HR-1 receptor, that shows 27% identity and 25% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a cDNA clone (see V04131) obtained from a Chaimed host cells, and used in a claimed method for identifying CC compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or caplastic anaemia, neutropaenia or cytotoxic treatments for cancer. CC dragnose predisposition to lowered resistance to infection, asthma, callergic or haematopoietic disorders, e.g. where induced by AIDS, can antagonists, e.g. antibodies or HR-1 receptor fragments, can coverexpression. The antibodies can also be used to determine HR-1 covered resistance to infection, asthma, cc sequence 380 AA;
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밁 Ş 밁 ş 밁 밁 ş 밁 Ş Query Match 12. Best Local Similarity 26. Matches 107; Conservative 232 HIKNLSFHND----DLYVQWENPONFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF 184 CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP 173 C-ENIFREGOYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP 70 ----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124 10 LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF 67 --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTATVENETY 293 ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ 172 SHFGDKQDKKIAPETRRSI------EVPLNERICLQVGS----QCSTNESEKPSILV 114 LYTELISTIFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEY- 70 12.7%; Score 295.5; DB 1; 26.0%; Pred. No. 8.6e-20; tive 63; Mismatches 169; Length 380; Gaps 231 241 183 11 20;

Search completed: January 19, 2000, 20:00:53 Job time: 8948 sec

B & B &

340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGD 391

-GFILILVIFVTGL--LLRKPNTYP-KMIPEFFCD 379

294 TLKTTNETRQLCFVV------RSKVNIYC-SDDGIWSEWSDKQCWEGEDLSKK 339

ERNVENTS---CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM-----SIGKK 339

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein , protein search, using sw model

Run

9 ::

January 19, 2000, 14:58:48; Search time 71.05 Seconds (without alignments) 283.481 Million cell updates/sec

Title: Perfect score: Sequence: US-09-077-817-4 2324

MEWPARLCGLWALLLCAGGG......QTKEETDSVVLIENLKKASQ 427

Searched: 142080 seqs,

47169319 residues

Scoring table:

BLOSUM62

Database PIR_62:*

Word size : 0

Number of hits that pass the threshold

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142080

pir1:*
pir2:* pir3:*

and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

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6	853	808	878	968	378	896	378	719	1092	333	830	396	897	622	918	630	808	, 303	292	616	581	310	412	610	610	831	369	369	373	400	335	333	396	420	415	Length D	
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	100254	S32823	A40091	I56563	S50040	A35782	A40266	JC2181	JX0312	S13684	I50455	S22909	A39255	A40144	A36337	I51086	I53269	I77524	177525	A30304	I45971	A29884	A41070	A36116	A34631	JQ1655	A42565	149280	A55718	S06945	A40267	S21053	S21050	S21052	S12357	IĐ	
20ma (00 to 7 to 1 to 20 to 2		somatotropin recep	interleukin-3 rece	interleukin-3 rece	granulocyte-macrop	cytokine receptor	interleukin-3 rece	differentiation-st	differentiation-st	granulocyte-macrop	prolactin receptor	interleukin-3 rece	cytokine receptor	prolactin receptor	Q										lactogen receptor	e				granulocyte-macrop	interleukin-5 rece	Description	*				

interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 *sequence_revision 10-Nov-1995 *text_change 20-Feb-1998 C;Accession: S21052; A46175 R;Murata, Y; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.

RESULT S21052

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*.	557	286	634	508	638	638	917	918	1097	638	
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	interferon alpha r	granulocyte-macrop	somatotropin recep	erythropoietin rec	somatotropin recep	somatotropin recep	glycoprotein 130 -	interleukin-6 sign	leukemia inhibitor	somatotropin recep	

ALIGNMENTS

Q C; Accession: S12357 R; Takaki, S.; Tominaga EMBO J. 9, 4367-4374, Ś Ĝ QΥ 밁 Ϋ́ D B 밁 3 ß A;Cross-references: GB:D90205; NID:g220465; pID:d1014936; PID:g220466 C:Keywords: cytokine receptor; transmembrane protein A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-415 <TAK> C:Species: Mus musculus (house mouse)
C:Date: 21-Nov_1993 #sequence_revision 10-Nov-1995 #text_change 20-Mar-1998 A; Accession: S12357 k_i . Title: Molecular cloning and expression of the murine interleakin-5 receptor. k_i . Reference number: \$12357, MUID: 91092260 interleukin-5 receptor - mouse Query Match
Best Local Similarity
Matches 97; Conserv 310 206 198 EQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQN-FISR 256 317 NKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKII---257 148 VSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPRTFINSKGF 205 1i0 SYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDLTKVKDSSF 197 266 CFNYELKIYNTKNG-----HIQKEKLIANKFISKIDDVSTY-----SIQVRAAV 309 88 HEGYAASVRTILKSSHTTLASSWVSAELKAPPGSPGTSVTNLTCTTHTVVSSHTHLRPYQ 147 91 NERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNL------ 140 29 PPV-NFTIKATGLAQVLLHWDPN-DQEQRHVDLEYHVKINAPQEDEYDTRKTESKCVTPL 87 33 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHF-GDKQDKKIAPETRRSIEVPL 90 CLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKT 316 EQLAYHINGSSKRAAIKPFDQLFSPLAIDQVNPPRNVTVEIESNSLYIQWEKPLSAFPDH 265 SSPCRMPGR-WGEWSQPIYVGKERKS-LVEWHLIVLP---TAACFVLLIFSLICRVCHLW Tominaga, Conservative A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu 13.7%;
23.9%; 74; Score 318; DB 2; Pred. No. 1.6e-17; 4; Mismatches 179 Length 415 Indels 56; Gaps 364 374 14;

65;

Gaps

16;

transmembrane

#status

predicte

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C;Accession: S21050; S78106
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the A;Reference number: S21050; MUID:92121815
                                                A; Molecule type: DNA
A; Residues: 1-396 < MT
                                                                                                                                                                                                                               C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision
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A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transme
F;1-20/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A46175; MUID:92357767
A;Accession: A46175
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A;Experimental source: clone lambda h5R.12
R;Tavernier, J; Tuypens, T; Plaetinck, G; Verh
Proc. Natl Acad. Sci. U.S.A. 89, 7041-7045, 1992
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                                                                                                                                                                                                                                                                              interleukin-5 receptor alpha chain precursor
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      ;Cross-references: EMBL:X61177; NID:g33839;
Experimental source: clone lambda h5R.27
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Best Local
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Residues: 333-420 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                                                                                                                                                                                                                                                                                                                                                                              ICHLWIKLFPPIPAPKSNIKDLFVTTN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                      --RLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLILSLICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVSAFPIHCFDYEVKIHNTRNG-----YLQIEKLMTNAFISIIDDLSKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERICLOV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102;
                                                     1-396 <MUR>
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g and expression of MUID:92121815
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Pred.
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No. 1.1e-15;
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                              PID: 933840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID: 933844
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                                                                                                                                                                                     Tominaga,
                                                                                                                                                                                                                                                                                lambda h5R.27) –
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                                                                                                                                                                                     Α.;
                                                                                                                                                                                                                                    05-Jun-1998
                                                                                                                                                                                     Takatsu,
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                                                                                                                                                                                                                                                                                                                                        R;Murata, Y.; Takaki, S.; Migita, M.; Kiku
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression
A;Reference number: $21050; MUID:92121815
A;Accession: $21053
F;1-20/Domain: signal sequence #status predicted <SIG>F;?1-33/Product: interleukin-5 receptor #status predicted <MAT>F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (coval
                                                                     A;Cross-references: EMBL:X62156; NID:g36465; PID:g36466 C;KF;ywords: alternative splicing; cytokine receptor; gl
                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-128,'I',130-333 <MUW>
                                                                                                                                                         A: Peference number: A: Accession: S78107
                                                                                                                                                                                   submitted to the EMBL Data A: Peference number: S78107
                                                                                                                                                                                                                                                A; Rostidues: 1-333 AMUR>
A; Cross-references: EMBL: X62156; NID: g36465;
A; Cross-references: clone lambda h5R.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 *sequence_revision 06-Feb-1998
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submitted to the EMBL Data Library, July
A;Reference number: $78106
A;Accession: $78106
                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A: Residues: 1-333 < MU
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C;Keywords: alternative splicing; cytokine receptor; gl:
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-128, 'I', 130-396 <MUW>
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                                                                                                                                                                                                                                  Murata,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
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Pred. No. 7.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Kikuchi,
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                                                                                                                                                                                                          September
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A; Molecule type: mRNA
A; Residues: 1-335 <TAV>
A; Cross references: GB:M75914;
C; Keywords: cytokine receptor;
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A;Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an, IL5-spec A;Reference number: A40267; MUID:92005669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision
C;Accession: A40267
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Best Local Similarity
Matches 82; Conserv
                 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 TVRIRVKTNKLCYEDDKLWSNWSQEMSIGK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR 200
                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                  32
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                   PVSAFPIHCFDYEVKIHNTRNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91
                                                  PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
                                                                                     TFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK
                                                                                                                          TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                                YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                                                                                                                                                                                                                                                             ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                                                                                                                                                                                                                                     PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-
                                                                                                                                                                                                   ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
                                                                                                                                                                                                                                        ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                                PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVSAFPIHCFDYEVKIHNTRNG----YLQIEKLMTNAFISIIDDLSKY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devos, R.; Cornelis, S.; Tuypens, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.9%;
ilarity 24.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            9.98;
24.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g186387; PID:g186388 transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                        ; Score 229; DB 2;
; Pred. No. 1.2e-10;
51; Mismatches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 230; DB 2;
; Pred. No. 9.6e-11;
51; Mismatches 145
               YLQIEKLMTNAFISIIDDLSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-Jan-1992 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QVKINAPK-EDDYETRIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 333;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van der Heyden, J.; Fiers, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A; Residues: 347-400 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .accession: A44474
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 DVQVPE VSSMCREAG-LWSEWSQPIYVGFSR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 TYRIRVKINKLCYEDDKLWSNWSQEMSIGKKR
                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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C:Genetics:
A:Gene: GDB:CSF2RA; CSF2R
A:Genetics: GDB:CSF2RA; CMIM:306250;
A:Genetics: GDB:C
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A;Map position: Xp22.32-Xp22.32; Yp11.3
C,Keywords: glycoprotein; growth factor receptor; transmembrane protein
E;1-22/Domain: signal sequence #status predicted <SIG>
E;23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status proficed <TMM>
E;32-346/Domain: transmembrane #status predicted <TMM>
E;346,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S06945; A41286; A44474
R;Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMEC J. 8, 3667-3676, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E;Molecule (M',377-400 <RAP)
E;Fesidues: (M',377-400 <RAP)
E;Cross-references: GB:S48539; NID:g258858; PID:g258859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R: Cappeld, G.; Willson, T. Genomics 14, 455-461, 1992
A;Title: Arrangement and 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;C/oss-ref:rences: EMBL:X17648; NID:g32087; PID:g32089
R:C/C:Sier; K.E; Wong, G.G.; Mathey-Prevot, B.; Nathan, D.G.; Sieff, Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
R:Title: L. furctional isoform of the human granulocyte/macrophage co.A;Reference number: A41286; MUID:91352066
A:Accession: A41286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qx'annlocyte-macrophage colony-stimulating factor receptor A
Machine Manes: GM-CSF receptor alpha chain; hemopoletic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            );Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                196 GTSREIGIQFFDSLLDTKKIERFNPPSNVTVRCNTTHCLVRWKQPRTYQKLSYLDFQYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 RNTSPDTNYTLYYWHRSLEKIHQCENIFRE-GQYFGCSFD-LTKYKDSSFEQHSVQIMVK 207
                                                                                                              263 EVN -- NSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLC 320
                                                                                                                                                                                                                                                                                                                                     208 DNACKIKPSF--NIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNF--ISRCLF-YEV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 TVAPASSLNVRFDSR-TMNLSWDCQENTTFSKCFL----TDKKNRVVEPRLSNNECSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERRICLHEGVTFEVHVNTSORGFOOKLLYPNSGREGTAAQNESCFIYNADLMNCTWARG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTAPRDVQYFLYIRNSKRRREIRCPYXIQDSGTHVGCHLDNLSGLTSRNY-----FLVN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNER:CLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 228; DB 2; llarity 22.4%; Pred. No. 1.7e-10; Onservative 82; Mismatches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.A.; Henke, A.;
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YNFPSSEPRAKHSVKIRAADVRIL
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C;ACCESSION. C;ACCESSION. C;ACCESSION. C;CAC, KOZAK, C.A.; Liu, r.
R;CAO, Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine
A;Title: Characterization of cDNAs encoding the murine
                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change
C;Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
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I49280
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A; Accession:
                                 A; Molecule type: DNA
A; Residues: 1-369 <CAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A55718
                                                                                                                                                                                                                        interleukin-2 receptor gamma chain precursor -
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A; Residues: 1-373 <HEN>
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R;Henthorn, P.S.; Somber
Genomics 23, 69-74, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 18-Aug-1995 #sequence_revision
C;Accession: A55718
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C:Species: Canis lupus familiaris (dog)
                Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 -- RDPREPRRQSTQKLKLQNLVIPWAP--ENLTLHNLSESQLELSWSN--RHLDHCLEHV 186
                                                                                                                                                                                                                                                                                                                      288 RIP 290
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                                                                                                                                                                                                                                                                                                                                                                                  SAOR-WSEWSHPIHWGSNTSKENPLFASEAVLIPLGSMGLIISLICVYYWLER----SIP
                                                                                                                                                                                                                                                                                                                                                                                                                   EDDKLWSNWSQEMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIIFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN----DDLYVQWENPQNFISRCLFYE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSFDLTKVKDSSFEQHSVQI 204
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            EMBL: U21795;
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25.1%;
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            NID:g727349; PIDN:AAA64279.1;
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Pred.
                                                                from GB/EMBL/DDBJ
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No. 7
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У.М.;
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           PID:g727350
                                                                                                               2 receptor
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A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, C;Superfamily: interleukin-2 receptor gamma chain C:Keywords: Cytchine receptor; duplication; glycoprotein; transmembrane profile production: signal sequence #status predicted <SIG> F;1-22/Domain: signal sequence #status predicted <SIG> F;2-365/Product: interleukin-2 receptor gamma chain #status predicted <MAN F;256-284/Pomain: transmembrane #status predicted <TMM> F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Description: receptor for interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C; Complex: The high affinity receptor is a heterotrimer of alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXT J. Immunol. 24, 3014-3018, 1994
A; Title: The murine interleukin-2 receptor gamma chain
A; Reference number: I53398; MUID:95104285
A; Accession: I53398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 130, 303-304, 1993
A;Title: Cloning and sequencing of the cDNA
A;Reference number: JN0775; MUID:93366191
A;Accession: JN0775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: Regulation of CD44-mediated A;Reference number: S37582 A;Accession: 337582
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A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration A;R:gference number: JN0592; MUID:93277575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1;
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A; Residues: 1-369 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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R:D:Santo, J.P.; Certain, S.; W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-350,'S',352-366,'S',368-369
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A; Residues: 1-369 < KUM>
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A; Residues: 1-369 <RE2>
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Best Local
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271 THNVFYYQEAKCENPEFERNVENTSCFMYPGYLPDTLN--TVRIRVKTNKLCYEDDKLWS
                                                                                    140
                                                                                                                                                                                                                    160 LYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQ-----IMVKDNAGKI
                                                                                                                                                                                                                                                                                                                  103 STNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPD---TNYT 159
                                                                                                                        214 KPSFNIVPLTSRVKPDPPHIKNLSFHN---DDLYVQWENPQNFISRCLFYEVEVNNSQTE
                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                 31
                                                               RRAVQKLNLQNLVIPRAP--ENLTLSNLSESQLELRWKS-RHIKERCLQYLVQYRSNRDR 196
                                                                                                                                                                                                                                                                         SANEDIKADLILTSTAPEHLSAPTLPLPEVQCFVFNIEYMNCTW----NSSSEPQATNLT
                                                                                                                                                                        LHYRYKVSD-----NNTFQECSHYLFSKEIT--SGCQIQKEDIQLYQTFVVQLQDPQKPQ 139
                                                                                                                                                                                                                                                                                                                                                                             76; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                 8.8%;
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                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                        Score 205.5; DB 2;
Pred. No. 9.1e-09;
3; Mismatches 121;
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C;Genetics:
A;Gene: GDB:IL2RG; SCIDX1; IMD4
A;Cross references: GDB:I34807; OMIM:308380
A;Map position: Xq13.1-Xq13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 30
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 30
A;Note: defects are associated with an X-linked form C;Superfamily: Interleukin-2 receptor gamma chain C;Keywords: cytokine receptor; duplication; immunodef
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R;Puck, J.M.; Deschenes, S.M.; Portu
Hum. Mol. Genet. 2, 1099-1104, 1993
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A;Title: Cloning of the gamma chain of the human IL-2 receptor A;Reference number: A42565; MUID:92335883
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Biol. Chem. 268, 13601-13608, 1993
Fittle: Characterization of the human interleukin-2; Reference number: A46591; MUID:93293887
Accession: A46591
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Title: The interleukin-2 receptor gamma chain maps to Reference number: I54332; MUID:94004847
Accession: I54332; Accession: 154332; Accession: Note that the second second
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Best Local Similarity 27.2%;
Matches 72; Conservative 44
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Residues: 1-369 <R
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Accession: A42565; A46591; I54332
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GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIG---KKRNSTLYITMLLIVPVIVA 357
                                                                                                                                                                     VQWENPQNFISRCL----FYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300
                                                                                                                                                                                                                                                                                                                                          DLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFH---NDDLY 244
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                                                                                    LNWNN--RFLNHCLEHLVQYRTDWDHSWT--
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                                                                                                                                                                                                                                                                                                                                                                                                                          EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGC-- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSF
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Pred. No. 1.7e-08;
4; Mismatches 101
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A;Experimental source: kidney C: Yeywords: glycoprotein; transmembrane protein F;1-23/Domain: signal sequence #status predicted <SIG>F;24-831/Product: prolactin receptor #status predicted <MAT>E;439-462/Domain: transmembrane #status predicted <TMM>F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site:
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Biochem. Biophys. Res. Commun. 168, 415-422, 1990 A; Title: Isolation and characterization of two novel A; Reference number: A34631; MUID: 90241201
                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
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A34631
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Siochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title; Double antenna structure of chicken prolactin
A;Reference number: JQ1655; MUID:93075121
                                                                   R; Zhang, R.; Buczko,
                                                                                           C; Accession:
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A; Residues: 1-831 <TAN>
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C; Species: Gallus yallus (chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 QFGSPY-NLTLETKRSANIMYLWAKWSPPLLADASSN----HLYHY----ELRIKPEEKE 176
                                                                                                                                                                                                                                                                              445 LGYLSSLICLIMSWTMYLKGYRMITFMLPPVPGP 478
                                                                                                                                                                                                                                                                                                                          353 PVIVAGATIVLL---LYLKRLKTIIF--PPIPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 INRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ-QTQYKMFSLN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 YEGCSEDLTKVKDSSEEQHSVQIMVKDNAGKIKPSENIVPLTSRVKPDPP-----HIKNL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 GAIIVLL---LYLKRLKIIIFPPIP 379
                                                                                                                                                                                                                                                                                                                                                                                                                   293 NTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 PNSCYFD--KKHTSFWTIYNTTVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 SIEVPLNERICLQVGSQCSTNE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-Sep-1993 #sequence_revision 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-----KPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGEEQVYECPD-YRTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWET-----ISVGVQTQCKINRLNAGMRYVVQVRCTLDPGEWSEWSSERHILIPSGQSPP
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                                                                 E.; Tsai-Morris, C.H.; Hu, Z.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.5%;
23.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 197.5; DB 2; Pred. No. 1.1e-07;
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                   rat ovarian lactogen receptor
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A:Title: Expression of two forms of prolactin
A;Reference number: A36116; MUID:91155946
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-610 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: A36116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin receptor 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar_1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <ZHA>
A;Cross-references: GB:M34083; NID:g205122; PID:g205123
A;Note: the authors translated the codon GAG for residue
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Best Local Similarity
Matches 68; Conserv
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NDFTLKDTTVWIIVAILSAVICLIMVWAVALKGYSMMTCIFPPVPGP
                               RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDP
                                                                                              AKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKK 339
                                                                                                                                                                                                                              KIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKP 228
                                                                                                                              EPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWEIHF---
                                                                                                                                                            DPP----HIKNLSFHNDDLYVQWENPQNFISR----CLFYEVEVNNSQTETHNVFYVQE 279
                                                                                                                                                                                             TTYECPDYKTSGPN-SCFF--SKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEP
                                                                                                                                                                                                                                                              KPEI--HKCRSP---DKET------FTCWWNPGTDGGLPTNYSLTYSKEGEK 65
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                                                             ----TGHQTQFKVFDLYPGQKYLVQTR-----CKPDHGYWSRWSQESSVEMP
                                                                                                                                                                                                                                                                                                                                          Conservative
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23.7%;
                                                                                                                                                                                                                                                                                                                                   8.1%; Score 189; DB 2; 1
23.7%; Pred. No. 3.4e-07;
tive 43; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.; Jolicoeur, C.;
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Pred. No. 2.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                    Length 610
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269
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                        F; 20-310/Product:
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C: Reywords: transmembrane protein F:1-19/Domain: signal sequence #status predicted <SIG>
                                                                 A; Malecule type: mRNA
A; Residues: 1-310 <BOU>
                                                                                                   A; Title: Cloning and expression of the rat A; deference number: A29884; MUID:88165059 A; Accession: A29884
                                                                                                                                                               R; Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Cell 53, 69-77, 1988
                                                                                                                                                                                                 prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
C;Lccession: A29884
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A29884
                                       A;Cross-references: GB:M19304; NID:g206364; PID:g206365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Crrss-references: EMBL:U07567; NID:g641963; A:Experimental source: Nb2-11C cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell
A:Reference number: A41070; MUID:92041834
A:30cession: A41070
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A; Residues: 1-412 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prolactin receptor Nb2 precursor - rat
C:Spacies: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
C:Accession: A41070; I55417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A) Molecule type: mRNA
A) Fosidues: 1-412 <ALI>
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Biol. Chem. 269, 26076-26082, 1994
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Best Local Similarity
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23.7%;
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Pred. No. 2.1e-07;
3; Mismatches 120
                                                                                                                                     prolactin receptor,
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Best Local Similarity
Matches 80; Conserv
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Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       168 EKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVK 227
                                             386 KEMFGDQNDDTLHWKKYDIY -- EKQTKEE 412
                                                                                                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                                    228 PDPPHIKNLSF---HNDD----LYVQWENPQN-----FISRCLFYEVEVNNSQT---E 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 NDFTLKDTTVWIIVAILSAVICLIMVWAVALKGYSMMTCIFPPVPGP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDP 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 EPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWEIHF--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 KIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 KPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLE 168
                                                                                             219 SPESSIQIPNDFPVKDTSMWIFVAILSAVICLIMVWAVALKGYSMVTCILPPVPGP-KI- 277
                                                                                                                                                                                           182 THFTLKQTQLKIFN----------LYPGQKYLVQIR------CKPDHGYWSEW
                                                                                                                                                                                                                                      271 THNVEYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNW 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 EKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 DPP----HIKNLSFHNDDLYVQWENPQNFISR----CLFYEVEVNNSQTETHNVFYVQE 279
                                                                                                                                                                                                                                                                                                                                                                                       70 TLIHECPD-YKTGGPNSCYF--SKKHTSIWKMYVITVNAINQMGISSSDPLYVHVTYIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 EKPKLV--KCRSPGK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 KPEI--HKCRSP---DKET------FTCWWNPGTDGGLPTNYSLTYSKEGEK 65
                                                                                                                                                                                                                                                                                         PEPP--ANLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFI---IQYEIRLKPEKATDWE 181
                                                                                                                                           SQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDPGKIF 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          er, M.A.; Schuler, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TGHQTQFKVFDLYPGQKYLVQTR-----CKPDHGYWSRWSQESSVEMP 222
-KGFDVHLLEKGKSEE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the bovine prolactin receptor and distribution of prolact MUID:93246019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 186; DB 2; Pred. No. 5.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ETFTCWWEPGADGGLPTNYTLTYHKEGE 69
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January 19, 2000, 14:58:50

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OM protein - protein search, using sw model

Run on: January 20, 2000, 06:19:55; Search time 35.05 Seconds (without alignments) 354.343 Million cell updates/sec

Title: Perfect score: Sequence:

BLOSUM62 US-09-077-817-4
2324
1 MEMPARLCGLWALLLCAGGG......QTKEETDSVVLIENLKKASQ 427

Scoring table:

Searched: 80000 seqs, 29085965 residues

Database : SwissProt_38:*

Word size :

Number of hits that pass the threshold : 80000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:

SUMMARIES

Result No. 1 2 3 3 4 6 6 7 8 8 9 9	· O · ON · P · N · F	Query Match 100.0 73.1 13.7 12.8 12.7 9.8 8.9 8.9	Length: 427 427 415 420 380 400 380 400 373 369 369 831			Description P7852 homo 09030 mus P21183 mus P21183 mus P21187 homo 014627 homo P15509 homo P40321 can1 P34902 mus P31785 homo 091994 mele
10 11 12	205.5 202 198.5 197.5 197	& & & & & & & & & & & & & & & & & & &	369 369 831 831		CYRG_MOUSE CYRG_HUMAN PRLR_MELGA PRLR_CHICK CYRG_BOVIN	P34902 P31785 Q91094 Q04594 Q95118
12 14 15	197 189 186		379 610 581		CYRG_BOVIN PRLR_RAT PRLR_BOVIN PRLR_RABIT	Q95118 P05710 Q28172 P14787
16 17 18	180 176 173 172.5		608 918 622			Q08501 Q91513 P40189 P16471
20 21 22	168 168 163		897 396 830	سو سو دج	CYRB_HUMAN IL3A_MOUSE PRLR_COLLI	. P329 0903
23 25 25	σ · σ		581 1092 378		PRLR_CEREL LIFR_MOUSE IL3R_HUMAN	Q282 P427 P269
26 28 28	157 149 146.5		896 878		CYRB_MOUSE IL3B_MOUSE GHR_CHICK GUB_BOUTN	P26955 P26954 Q02092
29 30 31	145 145 144.5 144		634 638 1097 918	بر بر تر بر	GHR_BOVIN GHR_HUMAN LIFR_HUMAN IL6B_RAT	P791 P109 P427 P401
	142.5 141 141 140 130	500000 500111	917 611 638 508		IL6B_MOUSE GHR_COLLI GHR_PIG GHR_RBIT EPOR_HUMAN GUB SUSEB	Q0056 Q0037 Q9037 P1994 P1994
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•	P24394 homo sapien			Q04790 bos taurus		

ALIGNMENTS

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RESULT 2

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ID 1131_MOUSE

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EMBL; U62858; AAB37127.1;
HSSP; P31785; 11LN.
MIM; 300119; -
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  Last sequence update)
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N REF. 3).
7 CRC32;
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SEQUENCE
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SIGNAL
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1- FUNCTION: BINDS II-13 WITH A LOW AFFINITY. TOGETHER WITH IL-ALPHA, CAN FORM A FUNCTIONAL RECEPTOR FOR II-13. ALSO SERVES ALIPHA, CAN FORM A FUNCTIONAL RECEPTOR FOR II-13. ALSO SERVES ALITERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR CHAIN FOR II-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities reguires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1)
13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
IL13RA1 OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:105052;
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                                                                                                                                                                                                                            Local Similarity
les 319; Conserv
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SIBUINT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPH.

SUBURIT: AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY)

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KII

TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL I

SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                       NCTLRYFSHFDDQQDKKIAPETHRKEELPLDEKICLQVGSQCSANESEKPSPLVKKCISP
                                                                              NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
                                                                                                                                                                                                                                                                                                                                   ΑĀ,
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                                                                                                                                                                                                                                                                                                                                                         103
1362
3382
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13. WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
BLANCON PROPERTY FOR IL-13. ALSO SERVES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                   48402 MW;
                                                                                                                                                                                                                                              73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Immunoglobulin domain; Signal POTENTIAL.
                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                            Score 1698.5;
Pred. No. 1.6e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE
POTENTIAL.
BY SIMILARITY.
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CYTOPLASMIC
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1.6e-123;
hes 64;
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Mus.
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
INTERLEXIN-5 RECEPTOR ALPHA CHAIN PRECURSO
  DOMAIN
DISULFID
DISULFID
                                                                      SIGNAL
                                                                                                                                          EMBL;
                                                                                                                                                 use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anuor send an email to license@isb-sib.ch).
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Mus musculus (Mouse).
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                                     TRANSMEM
                                                             CHAIN
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                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                              SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN THE CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CGF RECEPTORS. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPH
                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                              FUNCTION: THI:
BINDS TO IL-5
                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                       ON B-CELLS.
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                                                                               PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG PS00340; RECEPTOR_CYTOKINES_2; 1.
; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                           cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                   TOMINAGA
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                                                                                                                                         BAA14231.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                     IL5RA
                                                                                                                                                                                                                                                            TO IL-13 RECEPTOR ALPHA-2 CHAIN.
                                                                                                                                                                                                                                                                         BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
   415
339
361
415
152
193
                                                                                                                                                                                                                                                                                                                                                          IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                  Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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INTERLEUKIN-5 RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL). POTENTIAL). CYTOPLASMIC (POTENTIAL). BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                AND BASOPHILS.
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Mus.
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SEQUENCE
                                    SEQUENCE;
TAVERNIER J., DEVOS R., ETERS W., PLAETINCK S., A human high affinity
                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa:
Eutheria; Primates;
                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, 0
91-JUL-1993 (Rel. 26, 1
91-NOV-1997 (Rel. 35, 1
JUTERLEUKIN-5 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 92357767.
                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; $2372031.
                                                                                                         DEVOS R.;
                                                                                                                  TAVERNIER J., TUYPENS T.,
                                                                                                                                                               SCOTT H.S., GUO X.H., HOPWOOD J.J., "Structure and sequence of the humar genomics 13:1311-1313(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                    374
                                                                  "Molecular basis of the membrane-anchored and two
the human interleukin 5 receptor alpha subunit.";
eroc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                    365 TRLEPPVPAPKSNIKDL-------PVVTEYEKPSNETKIEVV 399
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97; Conservative
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26, Last sequence update)
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EPTOR ALPHA CHAIN PRECURSOR
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Catarrhini; Hominidae;
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  interleukin-5
                       CORNELIS S., TUYPENS T., VAN
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Pred. No. 2.4e-17;
4; Mismatches 179;
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                                               FORM).
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n alpha-L-iduronidase gene.";
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DOMAIN
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EMBL; M96651; AAA59151.1; -.
EMBL; M75914; AAA3611.1; -.
EMBL; A26249; CAA01793.1; -.
EMBL; A26287; CAA01731.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA BINDS TO IL-5.
-i- SUBBURIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an IL5-specific alpha chain
for GM-CSF.";
Cell 66:1175-1184(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLUBLE FORMS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
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PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
                                                                                                             ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL
                                                                                                                                                                                                                                                      PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
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                               TFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK
                                                             TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN
                                                                                            YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                                                                                                                                                                          ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL--- 140
                                                                                                                                                                                                                        PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT 82
                                                                                                                                                            ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN
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MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
; 75C19847 CRC32;
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DOMAIN

POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.

TRANSMEM

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RESULT 5
   EMBL; U70981;
EMBL; Y08768;
MIM; 300130;
                                                                       Receptor;
SIGNAL
                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                GUO J. MINVIELLE S.; to the EMBL/GenBank/DDBJ databases Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO: (IL-13), BUT NOT TO IL-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-RENAL CELL CARCINOMA;
MEDLINE, 96279273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DONALDSON D.D., WHITTERS M.J., FITZ L., NEBEN T., FINNERTY H., HENDERSON S.L., O'HARA R.M. JR., TURNER K.J., WOOD C.R., COLLINS Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING PROTEIN).
IL13RA2 CR IL13R.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13
                                            DOMAIN
                                                                                                     PROSITE;
                                                                                                                                                                           EMBL; X95302;
                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-!- SIMILARITY; BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a specific binding protein structurally related to the
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                                                                                                                   PF00041;
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                                                                                    Transmembrane;
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CAA70021.1;
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                                                                                                  RECEPTOR_CYTOKINES_2; 1.
363
363
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                                                                                    Glycoprotein; Signal
                                          INTERLEUKIN-13 RECEPTOR ALPHA-2 EXTRACELLULAR (POTENTIAL).
                                                                        POTENTIAL.
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IL-5 receptor alpha
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Best Local
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                                                                                                                                                                                                                                                                 GMCR_HUMAN STANDARD; PRT; 400 AA. P15509; Q14429; Q14430; Q1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR CHAIN PRECURSOR (GM-CSF-R-ALPHA) (CDW116) (CD116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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SEQUENCE
                                                                                                                            MEDLINE; 90059966.

GEARING D.P., INING J.A., GOUGH N.N.
GEARING D.F., STAIN J.A., GOUGH N.N.
CEARDO J. 8:3667-3676(1989).
                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; C
Eutheria; Primates; C
                                            "Cloning and sequencing of the cDNAs encoding splicing derived variants of the alpha subunit
SEQUENCE OF
                                granulocyte-macrophage
                                                                                MEDLINE;
                                                                                           TISSUE-BLOOD;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             CSF2RA OR CSF2R.
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                                                                    EMANUEL P.D.,
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                     Biophys.
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                                                                                                       (GM-CSF-R-ALPHA-2
                                                                                                                                                                                                   (GM-CSF-R-ALPHA-1)
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                                                      ZUCKERMAN K.S.;
ing of the cDNAs encoding
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                      colony-stimulating
1223:306-308(1994).
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                                                                                                                                                   NICOLA N.A.;
r human granulocyte-macrophage
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                                                                                                       GM-CSF-R-ALPHA-3).
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                                 factor receptor.";
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EMBL D26627; 1
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MAKAGAWA W., KOSTGI H., MIYAJIMA A., ARAI K.I., YOKOTA T.,

"Structure: The gene encoding the alpha subunit of the h

gramulocute, macrophage colony stimulating factor receptor.

Implications for the evolution of the cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, GM-CSF-R-ALP
HERE) TO GM-CSF-R-ALPHA-3, ARE PRODUCED BY ALTERNATIVE
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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the European Bioinformatics Institute
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IS PROBABLY SOLUBLE.
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  SEQUENCE
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                                                                                                                                                            VARSPLIC
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D26618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSJU241; RECEPTOR_CYTOKINES_1; 1. PSJU340; RECEPTOR_CYTOKINES_2; 1.
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POTENTIAL.

IN CONTROL OF THE PROPERTY OF THE PROP
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EIT -> DDHLGGIHPRGRERLPRRGLDREGNYLRPRGCRN
                  R-ALPHA-3
                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
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                                         GMDISASATRGNCFLDDAVNLYIIFYVFI
                                                                                                                                                                                                                                         FOTENTIAL.
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    F5C2EF6D
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ELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Alternative
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    CRC32
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L outstation -
                                         GM-CSF-
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RESULT 7
CYRG_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                      INTERLEUKINS.

- I SUBGUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AN PROBABLY ALSO THE IL-13 RECEPTORS.

- I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN:

- I DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED SEVERE COMBINED IMMUNODEFICIENCY.

- I SEVERE COMBINED IMMUNODEFICIENCY.

- I SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                             P40321;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
CYTOKINE RECEPTOR CAMMA CHAIN) (IL-2R GAMMA CHAIN)
                                                                                                                                                                                                                                             Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                                       severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                  HENTHORN P.S., SOMBERG R.L., FIMIANI V.M.,
                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Canis familiaris (Dog).
Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                    "IL-2R gamma gene microdeletion demonstrates that severe combined immunodeficiency is a homologue of
                                                                                                                                                                                                                                                                                                            FELSBURG P.J.
                                                                                                                                                                                                                                                                                                                                                          FISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYRG_CANFA
                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPDPGKIFKEMFGDQN--DDTLHWKKYDIYE-KQTKEETDSV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-----WSSWSEAIEFGSDDGNLGSVYIYVLLIVGTLVCG-IVLGFLFKRFLRIQRLFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEDDKLWSNWSQEMSIGKKRNS--TLYITMLLIVPVIVAGAIIVLLLYLKRLKI-IIFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVHRKNTQPGTENLLINVSGDLENR------YNFPSSEPRAKHSVKIRAADVRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVN--NSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNTSPDINYTLYYWHRSLEKIHQCENIFRE-GQYFGCSFD-LTKVKDSSFEQHSVQIMVK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNAGKIKPSF--NIVPLTSRVKPDDPHIKNLSFHNDDLYVQWENPQNF--ISRCLF-YEV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTAPRDVQYFLYIRNSKRRREIRCPYYIQDSGTHVGCHLDNLSGLTSRNY-----FLVN
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90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 228;
Pred. No. 1.
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.9e-10;
                                                                                                                                                                                                                                                                                                               PUCK J.M., PATTERSON D.F.,
                                                                                                                                                                                                                                                                      Of.
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                                                                                                                                                                                                                                                                      human
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RESULT 8
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Best Local
                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECUF
                                                                                     Eukaryota;
Eutheria; F
                                                                                                      Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                  CYRG_MOUSE
P34902;
                 MEDLINE;
               SEQUENCE FROM N.A. MEDLINE; 93277575.
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SEQUENCE
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                              288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 SAOR-WSEWSHPIHWGSNTSKENPLFASEAVLIPLGSMGLIISLICVYYWLER----SIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 EDDKLWSNWSQEMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 PIP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 MVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN---DDLYVQWENPQNFISRCLFYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 PGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSFDLTKVKDSSFEQHSVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 SSSEPRP-TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCW--LQKEEIHLYETFVVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76;
                                                                                                                                                                                                                                                                                                                                                                                                                                            290
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                                                                                  Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR_CYTOKINES_1; 1.
RECEPTOR_CYTOKINES_2; FALSE_NEG
                                                                        Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%;
25.1%;
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Pred. No. 7.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EQSVDHRNSFSLPSVDGQKFYTFRVRSRYNPLCG
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N PRECURSOR (GA
) (IL-2R GAMMA
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                                                                                                                                                                  (GAMMA-C)
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KONDO M.,

TAKESHITA

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NAKAMURA M.,

SUGAMURA

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EMBL;
EMBL;
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PIR;
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EMBL;
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EMBL;
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                        INTERLEUKINS.

1. SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2
PROBABLY ALSO THE IL-13 RECEPTORS.

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF
                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                  entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The murine interleukin-2 receptor gamma chromosomal localization and expression i Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAO X., KOZAK C.A., LIU Y.J., NOGUCHI M., "Characterization of cDNAs encoding the m (IL-2R) gamma chain: chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurooncol. 26:231-239(19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIU R.K., DRO DOUGHERTY G.J.
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MEDLINE; 93366191.
KOBAYASHI N., NAKAGAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of the mouse interleukin 2 recedemonstration of functional differences receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        the adhesion protein CD44
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular mechanisms regulating he adhesion protein CD44.":
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                                                       L; X75337; CAA5301; JN0592; JN0592; JN0775; JN0775.
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                                   MGI:96551; IL2RG
                                                                                                                                                                                                               D13821;
U21795;
PF00041; fn3; 1.
TE; PS00241; RECEPTOR_CYTOKINES_1;
TE; PS00340; RECEPTOR_CYTOKINES_2;
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                                                                                                                                AAB32904.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COOPER D.L., DOUGHERTY S.T.,
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MBL outstation -
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231785;
U1-JUL-1993 (Rel. 26, Created)
U1-JUL-1993 (Rel. 26, Last sequence update)
U1-JUL-1993 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GA
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CARBOHYD
CARBOHYD
SEQUENCE
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CARBOHYD
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MEDLINE; 93293887.
NOGUCHI M., ADELSTEIN
"Characterization of t
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DOMAIN
                                                                 MUNAKATA H., NAKAMURA M., SUĞN "Cloning of the gamma chain of Science 257:379-382(1992).
                                                                                              TAKESHITA T.
                                TISSUE-LIVER;
                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; (
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                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                           Futheria; Primates;
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                                                                                                            MEDLINE: 92335883
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                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
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                                                                                                                                                                                                                                                                                                            KNLEDLVTEYQGNFSAW
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                                                                                                                                           Catarrhini;
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Pred. No. 9.4e
63; Mismatches
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  interleukin-2
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                                                                                                 KUMAKI S., TANAKA
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ANTIGEN).
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receptor

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gene.";
J. Biol. Chem. 268:13601-136
[3]
SEQUENCE FROM N.A., AND VARI
MEDLINE: 94004847
PUCK J.M., DESCHENES S.M., P
                                             MEDLINE: 94300093.
ISHII N., ASAO H., KIMURA Y., TAKESHITA T., N
KONNO T., MAEDA M., UCHIYAMA T., SUGAMURA K.;
"Impairment of ligand binding and growth sign
receptor gamma-chains in patients with X-link
immunodeficiency.";
MEDLINE; 95023932.
DISANTO J.P., RIEUX-LAUCAT
                                                                                                                          "Detection of three nonsense mutations and o
the interleukin-2 receptor gamma chain gene
differently affect the mRNA processing.";
Genomics 21:291-293(1994).
                                                                                                                                                                                                               "Interleukin-2 (IL-2) receptor gamma chain mutations in severe combined immunodeficiency disease result in the l high-affinity IL-2 receptor binding."; Eur. J. Immunol. 24:475-479(1994).
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"Sharing of the interleukin-2 (IL-2)
receptors for IL-2 and IL-4.";
Science 262:1874-1877(1993).
                                                                                                                                                                 MARKIEWICZ S., SUBT
DE SAINT BASILE G.;
                                                                                                        VARIANT XSCID
                                                                                                                                                                                    VARIANT XSCID LYS-68. MEDLINE; 94375038.
                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Interleukin-2 receptor gamma chain: interleukin-4 receptor."; Science 262:1880-1883(1993).
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RUSSELL S.M., KKEC
LELAND P., FRIEDM
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                    VARIANT XSCID ASN-39.
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Science 262:1877-1880(1993).
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LEONARD W.J.;
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                                       Immunol. 153:1310-1317(1994)
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J. Clin. In
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New Engl. J. Med. 335:1563-1567(1996).
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JONES A.M., CLARK P.A.,
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Hum. Genet. 96:427-432(1995).
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Tryest. 95:895-899(1995).
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MEDLINE; 95164726.
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enet. 99:677-680(1997).
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the interleukin-2 receptor gamma
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01-NOV-1997 (Rel. 35, Created)
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PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR
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    TISSUE-KIDNEY;
MEDLINE; 97057891.
ZHOU J.F., ZADWORNY
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PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
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EMBL; U22947; AAA75038.1; -.
EMBL; U22924; AAA75039.1; -.
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PITTS G.R., YOU S.K., FOSTER D.N., EL HALAWANI M.E.; Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gallopavo receptor during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning,
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-CVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              PF00041;
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                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                fn3; 4.
                                                                                                                                                                                                                                                                                                                                                          RECEPTOR_CYTOKINGS__,
mbrane; Glycoprotein;
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FIBRONECTIN TYPE-III.
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FIBRONECTIN TYPE-III.
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MBL outstation -
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181 QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP-----HIKN 121 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG 180 126 OPGSPV-NLTLETORYANIMYLWAKWSPPLLADASSN----HLYHY----ELRLKPEEKE 176 EWETVFVG----SIE-VPLNERICLQVGSQCSTNE---------SEKPSILVEKCISP 120 QP-::PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFSHFGDKQDKKIAPETRR 84 GPNSCYFD--KKHTSFWTVYNITVKATNEMGSNSSDPHYVDVTYIVQPDPPANVTLELKK PE----KPTITKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGEEQVYECPD-YRTA Similarity Conservative -- VQTQCKINRLNAGMRYVVQVRCMLDPGEWSEWSSERRILISGGLSP 8.5%; 59; Score 198.5; Pred. No. 9.3 Mismatches .3e-08 DB 1; 157; Indels Length 87; Gaps 284 230 20;

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                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochem. Biophys. Res. Commun. 188:490-496(1992).

Biochem. PHIS IS A RECEPTOR FOR THE ANTERIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chord
Neognathae; Galliformes;
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                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANAKA M., MAEDA K., OKUBO T., NAKASHIMA K., Double antenna structure of chicken prolact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PINRKPYLMLTWSPPPLADVRSGWLTLDYELRLKPEEGEEWETVFVGQ-QTQYKMFSLN- 401
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PS00340;
                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
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(Rel. 29, Last sequence update)
(Rel. 36, Last annotation updat
    LEGHORN; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PGKKYIVQIHCKP----DHHGSWSEWSSENYIEIPNDFRVKDMIVWI 443
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                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR_CYTOKINES_1; 2.
RECEPTOR_CYTOKINES_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata;
rmes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Repeat
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                                                                                                                                                                                                                                                                                            CYTOPLASMIC
                                                                                                                                                                                                       FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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Q95118;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
CYTOKINE RECEPTOR C
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CARBOHYD
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                                                  the
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                       -i- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL
PROBABLY ALSO THE IL-13 RECEPTORS.
-i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                      DNA Cell Biol. 15:453-459(1996).
-!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 96268473.
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chorda
Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GA
(INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA
   entities
                                                                                                                                                                                                                                        gamma gene."
                                                                                                                                                                                                                                                      YOO J., STONE R.T., SOLINAS-TOLDO S., FRIES R., BEATTIE C.W.; "Cloning and chromosomal mapping of bovine interleukin-2 receptor
                                                                                                                                                                                                                                                                                                                                    Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                   [L2RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 LGVLSSLICLIMSWTMVLKGYRMITFMLPPVPGP 478
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                                               European Bioinformatics Institute.
                                                                                                                                                                    INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP-----HIKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QP--PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFSHFGDKQDKKIAPETRR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFHADDLYVQWENPQNFISR----CLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIEVPLNERICLQVGSQCSTNE-------SEKPSILVEKCISPP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPGSPV-NLTLETKRSANIMYLWAKWSPPLLADASSN----HLYHY----ELRIKPEEKE 176
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                                                                                                                                                                                                                                                                                                                                      Bos.
                non-profit institutions as long as its content and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PGKKYIIQIHCKP-----DHHGSWSEWSSENYIQIPNDFRVKDMIVWIV
 requires
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335 '
831 AA;
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335
94102
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   license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 197.5; DB 1; Pred. No. 1.1e-07; 59; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                 ta; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Bovoidea; Bovi
   agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
; B977BF07 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379
oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                               There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                               restrictions
                  and for
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                                                                                                                                                                                                                                                                                                         PRIR_RAT STANDARD; PRT; 610 AA P05710; Q63451; Q63723; Q62832; Q64274; Q63 01-NOV-1988 (Rel. 09, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PROLACTIN RECEPTOR PRECURSOR (PRI-R) (LACTO
                                                                                                               SHIROTA M., BANVILLE D., EDERY M., DJIANE J., KEL EEPRESSION of two forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_Receptor; Transmembrane; Glycoprotein; Signal.
  STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY; MEDLINE; 90241201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                      SEQUENCE FROM N.A.
                                                                                                       "Expression
                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 91155946.
                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWS------QEMSIGKKRN | :: | :| | :| :| :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STPAGTLDVSTLPLPKVQCFVFNVEYMNCTWNSSSEPQPN-NLTLHYGYRNFNGDDKLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPEGDPESA---VTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSL---EKIHQ 172
                                                                            Endocrinol. 4:1136-1143(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIIFPPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDHRHSFSLPSVDAQKLYTFRVRSRYNPLC-GSAQHWSDWSYPIHWGSNTSKENIENPEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEN-IFREGOYFGCSFDLTKVKDSSFEQHSVQIM-VKDNAGKIKPSFNIVPLTSRVKPDP
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                                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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290
379
256
256
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122
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171
                                        (LONG FORM AND SHORT FORM)
                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43037
                                                                                                             D., ALI S., JOLICOEUR C., KELLY P.A.; prms of prolactin receptor
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 197; DB 1;
Pred. No. 4.4e-08;
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FIBRONECTIN
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                                                                                                                                                                                                                                  Craniata; Vertebrata; Mammalia;
thi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                           (LACTOGEN RECEPTOR).
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                                                                                                                                                                                                                                                                                                                                                                                       Q63479;
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FALSE_NEG
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                                                                                                                                                       BOUTIN J.M.,
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                                                                                                                                                                                           lternative
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EMBL: M57668: AAA41938.1; -
EMBL: M34093; AAA79273.1; -
EMBL: L48060; AAA79274.1; -
EMBL: U34730; AAA92053.1; -
EMBL: M19304; AAA41937.1; -
EMBL: M74153; AAA41937.1; -
EMBL: W74153; AAA41946.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CLOming and expression of the rat prolactin receptor, a member of the growth hormone/prolactin receptor gene family.";

Cell 53:55-77(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAK LOCATION: TYPE I MEMBRANE
-1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS
SPLICING OF THE PRLR GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A prolactin-dependent i of prolactin receptor.";
J Biol Chem. 266:20110
                                                                                                                                                                                                     PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PS00241; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long of modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'NEAL K.D., YU-LEE L.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECULNCE FROM N.A. (FORM NB2).
MEDLINE, 95014432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 231-610 STOCCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and characterization receptor cDMA species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BANVILLE D., STOCCO R., MURTHY K.K., BOIE Y., KELLY P.A.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        FIR; A29884; A29884.
                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Swiss Institute of Bioinformatics
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                                                                                                                                                                                     Transmembrane;
splicing.
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2 1 610
20 229
230 253
254 610
20 117
119 222
31 41
70 81
54 54
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THIS IS A RECEPTOR FOR THE ANTERIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266:20110-20117(1991).
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              EXTRACELLULAR (BY SIM:
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CYTOPLASMIC (BY SIMILA
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                   PROLACTIN RECEPTOR
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                                                                                                                     SIMILARITY)
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Best Local Similarity 23.7%;
Matches 68; Conservative 4
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Q28172;
Q1-NOV-1997
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VARSPLIC
                                                    SCOTT P., KESSLER M.A., SCHULER L.A.;

Molecular cloning of the bovine prolactin receptor and
of prolactin and growth hormone receptor transcripts in
utero-placental tissues.";

Mol. Cell. Endocrinol. 89:47-58(1992).

-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUIT
                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
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                                                                                                                                             SEQUENCE FROM N.A. TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                      BOVIN
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      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
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MISSING (IN FORM NB2).

V -> A (IN REF. 2).

G -> V (IN REF. 2).

E -> K (IN REF. 1).

O -> E (IN REF. 2).

A -> G (IN REF. 2).

A -> G (IN REF. 2).

A -> K (IN REF. 2).
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Pred. No. 3.3e-07;
3; Mismatches 120
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TGSPSKYKVDLYLALPGGFQKLDNAGELDY
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EVKQLKDKKTYLWVKWSPPT -> DYRWEVSCHQEALPKSA
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                                                         PITUITARY HORMONE
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the European Bioinformatics Institute
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                         386 KEMFGDQNDDTLHWKKYDIY--EKQTKEE
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----KGFDVHLLEKGKSEE
                                                             SQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK----IIIFPPIPDPGKIF
                                                                                                             THNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNW
                                                                                                                                                      PDPPHIKNLSF---HNDD-----LYVQWENPQN-----FISRCLFYEVEVNNSQT---E
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                                              SPESSIQIPNDFPVKDTSMWIFVAILSAVICLIMVWAVALKGYSMVTCILPPVPGP-KI-
                                                                                         THETLKQTQLKIEN-------LYPGQKYLVQIR-----CKPDHGYWSEW
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RECEPTOR_CYTOKINES_2; 1.
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; Pred. No. 5.3e-07;
44; Mismatches 115
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BY SIMILARITY.
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RRR COCCUPATOR
                                                                                                                                                RESULT
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01-APR-1990 (Rel.
15-JUL-1998 (Rel.
                   SEQUENCE FROM N.A.
                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                 PRLR_RABIT
                                                                                                                                       RABIT
                                      Eutheria;
                                                                            PROLACTIN RECEPTOR
          ISSUE-MAMMARY
AMMARY GLAND;
89184578.
                                     Lagomorpha;
                                                                                                                             STANDARD;
                                                                                   14, Created)
14, Last sequence up
36, Last annotation
                                                                            PRECURSOR
                                     Leporidae;
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                                    Oryctolagus
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Proteins 27:459-468(1997)
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*HALABY D., THOREAU E., DJIANE J., MORNON J.P.;

*HOMOlogy_modeling of rabbit prolactin hormone complexed with
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PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DJIANE J.;
"Identification and sequence analysis of a second form of prolactin
receptor by molecular cloning of complementary DNA from rabbit
                  334 MSIGKKBNSTLY-ITMLLIVPVI--VAGAIIVLLLYLKRLKII--IFPPIPDP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
                                                                184
                                                                                                                                127
                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROSITE;
                                                                                                                                                                228
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
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                                                               -FAGQQTQ----
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SSIQIPNDFTMKDITVWIFVAVLSTIICLIMVWAVALKGYSMVTCIFPPVPGP 274
                                                                                            VFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQE 333
                                                                                                                                                             PDPPHIKNLSF---HNDD----LYVQWENPQNFISR----CLFYEVEV---NNSQTETHN 273
                                                                                                                                                                                             TITHECPD-YKTGGPNSCYF--SKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVE
                                                                                                                                                                                                                              KI-HQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVK 227
                                                                                                                                                                                                                                                              PDPP--VNLTLEVKHPEDRKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWETH- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00041;
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27.3%; Pred. No. 6.9e-07;
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FB6170B1 CRC32;
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BY SIMILARITY.
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

January 20, 2000, 06:37:46;

; Search (without 1074.609

time 24.34 Seconds alignments)
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Number of Word size Database : Searched: Scoring table:

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sp_archea:*

sp_fungi:* sp_bacteria:*

sp_invertebrate:* sp_human:*

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sp_plant:*

sp_rodent:*
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sp_vertebrate:*
sp_unclassified:*

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O1-MAY-1999 (TrEMBLrel. 10, I
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INTERLEUKIN-13 RECEPTOR.
                                                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U81379; AAD00510.1; -
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 98.6%;
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         GVLPDTLNTVRIRVKTNKLCYEDDKLMSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
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                                                   DFLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
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Q94655 plasmodium
O15770 plasmodium
O61210 caenorhabdi
O13221 homo sapien
C18985 cervus elap
Q92856 homo sapien
Q98921 gallus gall
Q98922 gallus gall
Q98923 gallus gall
Q98924 lucilia cup
Q70458 mus musculu
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O96435 drosophila
Q15426 homo sapien
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046386 mustela vis Q16354 homo sapien Q921a0 cavia porce Q63257 rattus norv P79203 ovis aries Q18245 caenorhabdi Q14632 homo sapien Q99650 homo sapien

046561 ovis aries 075462 homo sapien 057519 xenopus lae 016564 homo sapien 064146 rattus norv 070535 rattus norv

046600 bos taurus

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SUMMARIES

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Q14633;
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Q1-NOV-1996 (TIEMBLITEL 0:
Q1-NOV-1998 (TIEMBLITEL 0:
Q1-NOV-1998 (TIEMBLITEL O:
Q1-NOV-1998 (TIEMBLITEL O:
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097597;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
     Homo
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;
"Biological activities of interleukin-13 on bovine lymphocytes:
implications for signaling through IL-13Ral.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF074402; AAC98147.1; -.
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  sapiens (Human):
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Pred. No. 3.9e-133;
7; Mismatches 37;
                                                                                                                                                                          PRT;
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Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
                                                                          DONALDSON D.D., HENDERSON S.L.,
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Eutheria; Rodentia; Sciurogna
                                                                                                                                                                                               01-NOV-1998 (TremBLrel. 08, 01-NOV-1998 (TremBLrel. 08, 01-NOV-1998 (TremBLrel. 08, IL-13 RECEPTOR ALPHA 2.
                                                                                                                                                                                                                                                             088786 PRELIMINARY;
 EMBL; U65747;
                                                                                                                   STRAIN-C3H/HEJ;
                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                     088786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X61176; CAA43483.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Eutheria; Primates;
                                     "The murine IL=13 receptor alpha characterization, and comparison
                                                               COLLINS M.;
                                                                                                       MEDLINE; 98391042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURATA Y., TAKAKI S., MIGITA M., KIKUCHI "Molecular cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PERIPHERAL BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLINE;
                                                                                                                                                                                                                                                                                                                                    364
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             Immunol.
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                                                                                                                                                                                                                                                                                                                                                       --RLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVL 418
                                                                                                                                                                                                                                                                                                                                                                                      DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLILSLICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                              TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PON-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                         PVSAFPIHCFDYEVKIHNTRNG-----YLQIEKLMTNAFISIIDDLSKY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERICLOV-----GSOCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
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420 #
            161:2317-2324(1998).
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AAC33240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 47670 MW;
                                                                          WHITTERS M.J., FITZ L., O'HARA R.M. JR., BEIER I
                                                                                                                  TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                       Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%;
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                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 294.5; DB 4;
Pred. No. 6e-18;
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INTERLEUKIN-5 REC
247AB980 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                     2: mc
                                                 molecular cloning
                                                                                                                                                                                                                                                                   383
                                      murine IL-13
                                                                           D.R., TURNER
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                                                                                                                                                                                                          update)
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                                      receptor alpha
                                                                          FINNERTY K.J., WOO
                                                                                                                                                          Mammalia;
Mus.
                                                                             MOOD
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                                                                           C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                368
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RESULT
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Best Local
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q14631
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;
"Molecular cloning and expression of the human interleukin 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PERIPHERAL BLOOD; MEDLINE; 92121815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTERLEUKIN-5 RECEPTOR TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQLQNIVKPLPPEFLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YYWHRSLEKIHQCENIFR-EGQYFGCSFDLTKYKDSSFEQHSVQIMVKDNAGKIKPSFNI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-TNGSEVQSPWIEASYGISDEGSLETKIQDMKCIYYNWQYLVCSWKPGKTVYSDTNYTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSTNESEKPSILVEKCIS-PPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKPPVVIEKFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNKGIEGKIRTHLSEH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNPP-----EGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNE----RICLQVGSQ 101
                                                            ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN
                                                                                                 ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                       PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT 82
                                                                                                                                                                             PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDMKLKR---RANESEDLCFFV-------RCKVNIYC-ADDGIWSEWSEEECWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPLTSRVKPDPPHIKNLSFHND-DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFWYEGLDHALQCADYLQHDEKNVGCK--LSNLDSSDYKDFFICVNGSSKLEPIRSSYTV
                                                                                                                                                                                                                                                                                                                                                                                                X61177;
                                                                                                                                                                                                                    98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Med. 175:341-351(1992).
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    SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
                                                                                                                                                                                                                                                                                                                   396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation updat-
- RECEPTOR TYPE 2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                CAA43484.1;
                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                       396
                                                                                                                                                                                                                                                                                                                   44998 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini;
                                                                                                                                                                                                                                                                                                                                                         20
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Pred. No. 2.2e-17;
4; Mismatches 156;
                                                                                                                                                                                                                                    Score 282.5; DB 4;
Pred. No. 6.3e-17;
                                                                                                                                                                                                                                                                                                                   INTERLEUKIN-5 RECEPTOR 85FBF684 CRC32;
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i; Hominidae;
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01-MAY-1959 (TIEMBLIEL 10, C

01-MAY-1959 (TIEMBLIEL 10, I

01-MAY-1999 (TIEMBLIEL 10, I

INTERLEUKIN-5 RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and Characterization of the receptor alpha cDNA."; submitted (APR-1996) to the EMBL/GenBEMBL; U55215; AAD09361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Receptor.
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                                                                                  SRLSIQWQKPVSAFPIHCFEYEVKICNTKD-----YYQVEKTTTNAFVSTTDGVSKY--
                                                                                                                          DDTTYQWENPQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMV
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-SIQVRAAVSPHC-RAMGLWSKWSQPVYVGKEKKP--IAGWFLITLTAVLCF
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Pred. No. 1.2e-16;
5; Mismatches 186;
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Best Local Similarity 24.5%.
Matches 81; Conservative
                      Q14431 PRELIMINARY;
Q14431;
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01-NOV-1996 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
GM-CSF RECEPTOR.
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SEQUENCE
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MEDLINE; 92121815
MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., 1
"Molecular cloning and expression of the human interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
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                                                                                                                                                                                                                            DVQVRAAVSSMCREAG-LWSEWSQPIYVGK
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333 AA;
                                                                                                                          PRELIMINARY;
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333 S
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                                       Last sequence update)
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SOLUBLE INTERLEUKIN-5 RECEPTOR
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Query Match
tissues.";
Endocrinology 138:3187-3194(1997).
EMBL; AF027403; AAB83999.1; -
EFAM; PF00041; fn3; 2.
SEQUENCE 296 AA; 33854 MW; 8B4
                                                                                                                                                                                                                         Bos taurus (Boyine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
Boyinae; Bos.
                                                                                                                                                                                                                                                                                                          01880):
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PROLACTIN RECEPTOR SHORT FORM.
                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 97375450. SCHULER L.A., NAGEI
                                                                                                           SCHULER L.A., NAGEL R.J., GAO J., "Prolactin receptor heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "REFORM THE CONTROL OF THE PREVOT B., NATHAN D.G., SIEF "A functional isoform of the human granulocyte/macrophage colony-stimulating factor receptor has an unusual cytoplasmic domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                            018880
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EMBL; M64445; AAA35908.1; -.
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Eutheria; Primates;
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Pred. No. 1.4e-11;
75; Mismatches 178;
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093404;
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Oreochtomis mossambicus (Mozambique tilapia) (Tilapia mossambica)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygi
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha
Perciformes; Labroidei; Cichlidae; Tilapia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHIRAISHI K., MATSUDA M., MORI T., TETSUYA H.;
"Expression of prolactin and cortisol receptor gene in stages of tilapia (Oreochromis mossambicus).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF080247; AAC31825.1;
PFAM; PF00041; fn3; 2.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
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                                                                                                                                                                        NVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITM- 349
                                                                                                                                                                                                                                                                                       QWENPQNFISR----CLFYEVEV----NNSQTETH-----NVFYVQEAKCENPEFER
                                                                                                                                                                                                                                                                                                                                                                                                      TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDD----LYV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEITCRSPEKETFTCWWKPGSDGGLPTTYALYYRKEGSDVVHECPDYHTAGKN-SCFFN- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPP--ANLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFI---IQYEIRLKPEKATDWE 181
AYLHREKSVWILVVVFSAFILLILIWLIQMNSHSLKHCMLPPVPGP
                                                                                                                                                                                                                                 SWEPPHKADTRSGWITLIYELRVKLEDEESEWENHAAGQQKMFNIFSLRSG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSL 167
                                                         -----KRLKIIIFPPIPDP
                                                                                                                                                                                                                                                                                                                                             -KNDTLIWVSYNITVVATNALGKTYSDPVDIDVVYIVKPHPPEKLEVTVMKDQGWPFLRV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDPPHIKNLSF---HNDD-----LYVQWENPQN-----FISRCLFYEVEVNNSQT---E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%;
llarity 22.4%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39203 MW;
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                                                                                                                  -GTYLIQVR----CKPDHGFWSEWS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 177; DB 13;
Pred. No. 8.9e-08;
40; Mismatches 104
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41; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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274
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                                                                                                                  STSYVKVP 228
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                                                                                         RESULT 12
075469
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01-NOV-1598 (TIEMBLIE1 08, 01-NOV-1598 (TIEMBLIE1 08, 01-MAY-1999 (TIEMBLIE1 10, CYTOKINE-LIKE FACTOR-1 PRECUCLE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
SEQUENCE
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Eukeryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukeryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       046561
                                                                                                                                                                                                                                                                                272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIGNON C., DJIANE J.;
Submitted (JAN-1998) to the
EMBL; AF041257; AAB96795.1;
FFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."; J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98001468.
SIGNON C., BINART N.,
DJIANE J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUY-1978 (TIEMBLIEL 06, Created)
01-JUN-1993 (TIEMBLIEL 06, Last sequen
01-MAY-1994 (TIEMBLIEL 10, Last annota
PROLECTIN RECEPTOR LONG FORM PRECURSOR.
                                                                              €75462
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                                                                                                                                                                                                                                                                                HNVTTVQEAKCENFEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWS
                                                                                                                                                                                                                                                                                                            PEPP - - VNLTLELKHPEDRKPYLWIKWSPPTLTDVKSGWFS - - IQYEIRLKPEKATDWET
                                                                                                                                                                                                                                                                                                                                                             TLIHECPD-YKTGGPNSCYF--SKKYTSIWKMYVITVSAINQMGISSSDPLYVDVTYIVE
                                                                                                                                                                                                                                                                                                                                                                                       EKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVK 227
                                                                                                                                                                         EMEGDONDDTLHWKKYDIY--
                                                                                                                                                                                                  PESETUIFNDFPVKDTSMWIFVGVLSAVICLIMVWAVALKGYSMVTCILPPVPGP-KI--
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581 AA;
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             PRECURSOR
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                                                                                                                                                                       EKOTKEE
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                       Last sequence up
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Last sequence up
                                                   Created)
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PROLACTIN RECEPTOR LONG

6792A7C7 CRC32;
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Homo sapiens

(Human).

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RESULT 13
057519
ID 057519
AC 057519
DT 01-UNAY
DT 01-WAY
DE GP130P
GN XGP130P
GN XGP130
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Best Local 9
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Best Local
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057519;
01-JUN-1998
01-JUN-1998
01-MAY-1999
                                                                                                                                                                                CHEN J., GRACE A., CHIEN K.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF041845; AAC03531.1; -.
PFAM; PF00041; fn3; 4.
SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GRETENER D. MENOUD L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.; "CLF-1, a Novel Soluble Protein Shares Homology With Members Cytokine Type-I Receptor Family."; J. Immunol. 0:0-0(1998).

J. Immunol. 0:0-0(1998).
EMBL: AF059293; AAC28335.1; -
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Eutheria; E
[1]
                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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  123 GDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTL-YYWHRSLEKIHQCENIFREGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SNQTSC-RLAGLKPGTVYFVQVRCNPFGI-YGSKKAGIWSEWSHPTAASTPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLSFHNDDLYVQWENP---QNFISRCLF---YEVEVNNSQTETHNVFYVQEAKCENPEFE
| | | | :| :| : | | | :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEGDPESAVTELQCIWHNLSYMKCSWLPGRN--TSPDTNYTLYYWHRSLEKIHQCENIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV---HGDPPGATAEGLYWTLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDK--LWSNWSQEMSIGKKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGPH-SCHIP----KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGQYFGCSFDLTKVKD-SSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP---HIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GRRLPPELSRVLNA---STLALALANLNGSRQRSGDNLVCHARDGSILAGSCLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGDKQDKKIAPETRRSIEVPLNERICLQV----GSQCSTNE-----SEKPSILVEKCISP 120
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422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TremBLrel. 06, Created)
(TremBLrel. 06, Last sequence update)
(TremBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                             99003 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%;
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                                                                            7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                   32;
                                                Score 164; DB 13;
Pred. No. 4.1e-06;
32; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 169.5; DB 4; Length 422; Pred. No. 5.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOKINE-LIKE FACTOR-1.
; 877F9BC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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ea; Pipidae;
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Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
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Best Local Similarity
Watches 65; Conserv
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Q16564;
Q16-004-1096 (TEMBLICAL 01, C
Q1-NOV-1096 (TEMBLICAL 01, I
Q1-NOV-1998 (TEMBLICAL 08, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of a potentially soluble receptor for Nucleic Acids Res. 18:718-7178(1990).

EMBL; M73832; AAA35909.1; -.

EMBL; X54935; CAA38697.1; -.

Signal; Alternative splicing POTENTIAL.
SIGNAL: 1 22 GM-CSF RECEPTOR.
CHAIN 23 33 AA; 38438 MW; 48178079 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91376112.

RAINES M.A., LIU L., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE D.W.;

"Identification and molecular cloning of a soluble human

granulocyte-macrophage colony-stimulating factor receptor.";

proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91088339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alomo sapiens (Human).

Alomo sapiens (Human).

Alomo sapiens (Human).

Alomo sapiens (Human).

Alomo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASHWORTH A., KRAFT A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                       263 EVN--NSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 TQPPVTNLSVSVENLCTVIWTWNPPEGAS-SNCSLWYFSHEGDKQDKKIAPETRRSIEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 TVAPASSLNVRFDSR-TMNLSWDCQENTTFSKCFL----TDKKNRVVEPRLSNNECSC
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                                                                                                                                                                                                                                                                                                                                                                                                     LNERICLOVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPG
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.DVHRKNI'QPGTENLLINVSGDLENR--
                                                                                                              GTSREIGIQFFDSLLDTKKIERFNPPSNVTVRCNTTHCLVRWKQPRTYQKLSYLDFQYQL
                                                                                                                                                                     DNAGKIKPSF--NIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNF--ISRCLF-YEV
                                                                                                                                                                                                                                                                 RNTSPDTNYTLYYWHRSLEKIHQCENIFRE-GQYFGCSFD-LTKVKDSSFEQHSVQIMVK 207
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                                                                                                                                                                                                                               PTAPRDVQYFLYIRNSKRRREIRCPYYIQDSGTHVGCHLDNLSGLTSRNY-----FLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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20.5%; Pred. No. 1.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Mismatches
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Best Local Similarity 24.2%;
Matches 86; Conservative 5
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STRAIN-WISTAR; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00041; fn3; 2.
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"Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and its mRNA expression in vivo.";
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                               KRNSTLYITMLLIVPVIVAGAIIVLLLYL------KRLKIIIFPPIPDPGK 383
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Submitted (20-JAN-1997) J-F.M. Gauchat, Geneva Biomedical Research
Institute, Immunology, Glaxo, Research And Development, 14 Ch Des
Aulx, Plan-Les-Ouates, CH1228, SWITZERLAND
Location/Qualifiers
1. 4039
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1 (bases 1 to 4039)
Gauchat, J.F.M., Schlagenhauf, E., Feng, N.P., Moser, R., Yamage, M., Jeannin, P., Alouani, S., Elson, G., Notarangelo, L.D., Wells, T., Eugster, H.P. and Bonnefoy, J.Y.
A novel 4 kb IL-13Ra mRNA expressed in human B, T and endothelial cells, encoding for an alternate type two IL-4/IL-13R
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Gauchat, J.F.M.
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1 (bases 1 to 1572)

Aman, M.J., Tayebi, N., Obiri, N.I., Puri, R.K., Modi, W.S. and
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OGO Rockville Pike, Bethesda, M

Location/Qualifiers
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            /translation="MEMPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVEN LCTVINTWINDEBGASSNCSLWYESHFGDKOLKILAPETRRSLEVPLNERICLQYGSQG-STNESEKPELLVEKCISPPEGDPESAVIELQCIHNLLSYMKCSWLPGRNTSPDTNYTL YYWHRSLEKIHQCENIFREGQYFGCSFDLTKVGDSSFEQHSVQLMYKDNAGKIKPSFN IVPLTSRVKPDPPHIKNLSFHNDDLYVQMENPQNFISRCLFYEVEVNNSQTETHNVFY VQBAKCEMPETENVENTSCFMYPGVLLDTLNTVRIKVTNKLCYEDDKLMSNMSQEM SIGKKRNSTLYITMLLYPVYIVADALIVLLYLKRLKIIIFPPIPDPGKIFKEMFGDQ NDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ"

332 c 358 g 405 t
                                                                                                                                                                                                                                                      /function="cytokine receptor"
/note="IL-13 receptor: IL-13R or IL-13Ralpha; this protein together with the 140 kDa II-4 binding protein, IL-4R or IL-4Ralpha, can form a functional receptor for IL-13; IL-13R plus IL-4R is also one of the functional forms of the IL-4 receptor, the other is I!-4R plus the common cytokine receptor gamma chain"
                                                                                                                                                                      /product="interleukin-13
/protein_id="AAB37127.1"
/dh_xref="PID:g1695876"
/db_xref="GI:1695876"
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ho.mo sapiens"
/db_xref="taxon:9605"
/chromosom@="X"
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This sequence comes from Fig. 1.
Location/Qualifiers
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/db_xref="gi:gi911504"
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/translation="MARPALLOELLVLLLWTATVGQVAAATEVQPPVTNLSVSVENLC
TIIWTWSSPECANSNCTLRYFSHFDDQODKKIAPETHRKEELPLDEKICLQVGSQCSA
NESEKPSPLVKKCISPPGDPESAVTELKCIMHLSTWKCSWLFGRWTSPDTHYTLYY
WYSSLEKSRQCENIYREGQHIACSFKLTKVEBSFEHQNVQIMVKDNAGKIRPSCKIVS
UTSYVKEDPPHIKHLLLKNGALLVQWKNPQNFRSCCITYEVDNNUTQTDHHILEVEE
DKCQNSESDRNMEGTSCFQLFGVLALANYTTVRVTVKTYIKLCEDDNKLWSDWSEAQSIG
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95174767
U81380.2
Wada, M., Hisano, T. and Kuwano, M.
Direct Submission
Submitted (24 JUN-1999) Biochemistry, Kyusha
Medicine, Maidashi, Fukuoka 812-82, Japan
Sequence update by submitter
On Jun 24, 1999 this sequence version replace
Location/Qualifiers
1. 1099
                                                                                                       Wada, M., Hisano, T. and Kuwano, M. Direct Submission
Submitted (07-DEC-1996) Biochemistry, Kyumedicine, Maidashi, Fukuoka 812-82, Japan
2 (bases 1 to 1999)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IVPLISRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFY
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41..880
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Submitted (25-JUN-1998) Veterinary
Missouri-Columbia, W213 Veterinary
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AF074402.1
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227 c 216
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human STS
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                               STS; STS
 Eukaryota;
                     human.
            sapiens
                               sequence;
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sequence; primer;
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SHGC-34461,
 Metazoa;
Chordata;
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                               sequence
 Craniata;
                             tagged
                                                                       SITS.
 Vertebrata;
                               site
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 Mammalia;
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Best Local Similarity 96.6%;
Matches 310; Conservative ...
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CCTATCCACACAACATATCCGTATATATCCCCTCTACTTTACTTCCCCCCAAATTTAAAG
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Stanford University School of Medicine
Department of Genetics, M-344, Stanford
Tel: 415725987
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                     Prepared with primer pairs provided by Sande -- Washington University/Merck EST sequence Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer A: TCTGTTTATGCTTTTGGGGG
Primer B: GAAATGCCTCTCATTTCCCA
STS 61ze: 138
FGR Profile:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protocol:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers, R.M.
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/db_xref="taxon:9606"
/map="x"
23: 150
23: 42
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Taq Polymerase:
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Polymerization:
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Pred. No. 1.6e-59;
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                       ctactcgggaagctgaggcaggtgaattgtttgaacctgggaggttggaggttgcagtgag
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                                                                                                                                                                                                                                                          Similarity 82:399; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                          32479 a
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/db_xref="taxon:9606"
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34383 c 33834 g
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rimates; Catarrhini; Hominidae; Homo.
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6909: gap of unknown length
17944: contig of 11035 bp in length
17961: gap of unknown length
34519: contig of 16558 bp in length
34536: gap of unknown length
134578: contig of 100042 bp in length
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Pred. No. 1.1e-53;
0; Mismatches 65
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gap of unknown length 40855: contig of 1144 bp in length	f unknown lengt g of 859 bp in	of 922 b	of 599 b	37331: contig of 887 bp in length app of unknown length	ci unknown	ig of 680 b	ig of 1425	ig of 826 b	ig of 489 b	ig of 1599	ig of 827 b	ig of 744 b	cig of 1097	ig of 168 b	tig of 1096 b	26565: contig of 1285 bp in length gap of unknown length	gap of unknown length	gap of unknown lengt	gap of unknown lengt	gap of unknown lengt	gap of unknown length	gap of unknown lengtl	gap of unknown lengt	<pre>gap of unknown lengt contig of 675 bp in</pre>	gap of unknown lengtl contig of 995 bp in :	gap of unknown length 18783: contig of 500 bp in length	<pre>gap of unknown length 18283: contig of 746 bp in length</pre>	gap of unknown length 17537: contig of 935 bp in length	16602: contig of 601 bp in length	ig of 988 b	tig of 688 b	tig of 807 b	tig of 892 b of unknown	12626: contig of 577 bp in length gap of unknown length	gap of unknown lengt	gap of unknown lengt	gap of unknown length	
Query Match Best Local Similarity	* 96558	* 93788	* ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	* * * * * * * * * * * * * * * * * * *	0 00 00 00 00 00 00 00 00 00 00 00 00 0	* * 86467	* * 84747	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	* * * * CL	* 70070	7 1	* /5449	* 7377	*	* 72331	* 70472	69281	57768	- 66593	* 64632	* 63340	* 61385	* 59161	* 56900	* 55407	* * 54008	* * * (\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	* \$1601	* * *	1 d d d d d d d d d d d d d d d d d d d	* 40120	* 47481	* 45682	* 44182	* 43018	* 41931	40856	
6.3%; Score 253.6; DB 42; Length 141857; y 84.1%; Pred. No. 4.1e-52;	99457: contig of 2900 bp in le	96557: contig of 2770 bp in 1 gap of unknown length	gap of unknown length	21590: CONTIG OF 2154 bp in the control of unknown length	89436: contig of 1560 bp in gap of unknown length	gap of unknown length	86466: contig of 1720 bp in gap of unknown length	gap of unknown lengt	82113: contig of 1956 bp in gap of unknown length	80157: contig of 1288 bp in gap of unknown length	/8869: contig or 1961 bp in	76908: contig of 1460 bp in gap of unknown length	75448: contig of 1672 bp in gap of unknown length	gap of unknown length	gap of unknown length	gap of unknown length 72330: contig of 1859 bp in	gap of unknown 70471: contig of 1191	of 1513 bp in	67767: contig of 1775 in	66592: contig of 1961 b	64631: contig	63339: contig of 1955 b	61384: contig of 2224 b	59160: contig of 2261 b	56899: contig of 1493 b	55406: contig of 1399 l	54007: contig of 1016 bp in gap of unknown length	52991: contig of 1391 kg gap of unknown l	gap of unknown length	sap of unknown length	gap of unknown length	gap of unknown length	47480: contig of 1799 bp in	gap of unknown length	44181: contig	gap of unknown 1	gap of unknown 1	


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         Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 28, 1999 this sequence version replaced gi:5918360.
                                                          Submitted (29-SEP-1999) Wellcome Trust Genome Campus, Hinxton,
                                                                                   Direct
                                                                                                Babbage, A.
                                                                                                                           Eukaryota; Metazoa;
Eutheria; Primates;
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1999 this sequence version replaced gi:5918360. This sequence is unfinished and does not necessarily
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Catarrhini; Hominida
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Pred. No. 4.8e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent the correct sequence. Work on the sequence is in program and the release of this data is based on the understanding that sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJ785G19 Contig_ID: 00043 acc=AL035458 Length: 132647 bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
Submitted (08-OCT-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152878)
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/chromosome="20"
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SCORCE
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HSJ876B10
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Best Local Similarity
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**NOTE: This is a 'working draft' sequence.

**This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                   aaaactacaaaaattaactgggtggtggtggcgcgtgctgtaatcccagctactcgggaa 2006
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                                                                                                                                                                                                                                in unordered pieces.
AL117352
Submitted (30-SEP-1999) Wellcome Trust Genome Campus, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                            Direct Submission
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Best Local Similarity
Matches 276; Conserv
                                                                                                                                                                                    49361 TGGACCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGAGGCGGGCA 49420
                                                                                                                                                                                                                                                                                                                                                                                               49541 AGGCTGAAGCAAGAGAATCGCTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCCGAGATCG
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                                                                 2125 aaaacaaaacaaaaaa 2141
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* NOTE: This :-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phage etc.
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117352 Length: 1201 bp Unfinished: dJ876B10 Contig
acc-AL117352 Length: 19598 bp Unfinished: dJ876B10
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/db_xref="taxon:9606"
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87.1%;
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This sequence is unfinished and does not necessarily the correct seems of the correct seems 
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Pred. No. 1.
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acc-AL117352 Length:
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Search completed: January 20, 2000, 05:08:04 Job time: 9331 sec

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time 123.5 Seconds
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                                                                                                                                                                                                                                                                                                                                       consistences, which are receptors for interleukin-13 (IL-13) alpha receptor. The civention relates to new purified peptides comprising 380 or 427 amino control sequences, which are receptors for interleukin-13 (IL-13); the 380 conditions are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13R beta and alpha respectively. Out acquires high affinity when associated with the IL-4 conditions are designated IL-13R beta and alpha are used as conditions of heterozygosity and rearrangements, or chromosomal considered which can be used for production of recombinant IL-13R beta and alpha are used as conditions. They are also used for production of recombinant IL-13R beta and alpha which can be used for production of recombinant IL-13R beta and alpha which can be used for production of recombinant of allergy. Il-13. receptors are also used as IL-3 antagonists, specifically to consider therapy (blocking synthesis of IL-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression of IL-13 receptors, when coupled to a toxin also for treatment of overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R.

Sequence 4:09 BP; 1137 A; 826 C; 882 G; 1164 T;
                                                                                                                                                                                                                                                      Query Match 100.0%; Score 4009; Best Local Similarity 100.0%; Pred. No. 0; Matches 4009; Conservative C; Mismatches
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T85827;
T95827;
22-JUN-1998 (first entry)
Human interleukin-13 alpha receptor DNA.
Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.
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New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allerg
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Caput D, Ferrara P, Laurent P, Vita N; WPI; 97-319773/29.
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SUMMARIES

Database : Searched: Scoring table:

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311585 segs, 125096042 residues

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23-OCT-1995; AU-006135.
25-OCT-1995; AU-006135.
25-OCT-1995; AU-007276.
20-SEP-1996; AU-002208.
(AMYA-) AWRAD OPERATIONS PHILTON DJ. Metcalf D, NI-WPI; 97-259018/23.
DNA encoding animal haemopoletin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated by 1gE production

Claim 6; Page 52-54; 93pp; English.

DNA sequences (T66164 and T66165) respectively code for novel mouse and human haemoprotein receptors (W9821 and W09822) designated NR4 that comprise the interleukin-13 (IL-13) receptor alpha-chain. A human bone marrow cDNA library was screened with probes comprising nucleotides 82-840 and 840-1270 of murine NR4 cDNA, and a composite sequence for human NR4 was produced from isolated clones. The
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Best Local Similarity 99.6
Matches 1348; Conservative
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Sequence 1383 BP; 421 A; 292 C; 319 G; 351 T;
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Pred. No. 0;
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W09715663-A1.

OLAMAY-1997,
23-OCT-1995; AU-006135.
22-DEC-1995; AU-006135.
22-DEC-1995; AU-007276.

O9-SEP-1996; AU-007276.

H1.1:On DJ Metcalf D, Nicola NA, Willson T, Zhai K WPI; 97-259018/23.

E P-PSDB; W09821.

Interloukin-13 - useful to treat asthma, allergy or Claim 6; Page 48-50; 93pp; English.

DNA sequences (T66164 and T66165) respectively code and human haemoprotein receptors (W09821 and W09822).
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                                                                                                                                                                                                                                   e interleukin-12 receptor alpha chain NR4 DNA.
haemoprotein receptor; interleukin-13 recepto
kine; allergy; asthma; therapy; ss.
                                                                                                                                                                                                                                                                                                           GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA
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142 . .1338
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for novel mouse
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that comprise the interleukin-13 (IL-13) receptor alpha-chain. To cobtain the mouse sequence; genomic DNA prepd. from embryonal stem cells was screened with oligonucleotides encoding an amino acid sequence (WSDWS) found in many haemoprotein receptors. The genomic clone was used isolate NR4 cDNA clones from WEHI-3B cells, peritoneal macrophage, bone marrow, skin and kidney libraries, and composite sequence for mouse NR4 was produced. The availability of genetic sequences for NR4 permits the development of a range of agents capable of modulating the activity of IL-13 and related cytokines such as interleukin-4 for the treatment of altergy, asthma of ther conditions relating to IgE. The genetic sequences can also be used in prodn. of recombinant NR4 or fusion proteins including NR4.

Sequence 1383 BP; 416 A; 296 C; 315 G; 350 T;
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1078; Conserv
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                                                          acctctccttccacaatgatgacctatatgtgcaatgggagaatccacagaattttatta
                                                                                                                                                                                        NNAGTTTTGAACATCAGAACGTTCAAATAATGGTCAAGGATAATGCTGGGAAAAATTAGGC
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                                                                                                               CATCCTGCAAAATAGTGTCTTTAACTTCCTATGTGAAACCTGATCCTCCACATATTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAGTGCATCTCACCCCCTGAAGGTGATCCTGAGTCCGCTGTGACTGAGCTCAAGTGCA
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Nucleic acids encoding novel secreted proteins - useful as, e.g. anti-infianmatory, immuno-stimulatory or suppressing agents Claim 45: Page 80-81; 110pp; English.
The sequence is that of an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or emeliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers for tissues, molecular weight markers for gels, primers or probes, for nutrition as carbon, nitrogen or carbohydrate source. They can also be used as a cytokine for cell proliferation and differentiation activity, used as a cytokine for cell proliferation and differentiation activity,
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04-OCT-1996; US-726237.
(GEMY) GENETICS INST INC.
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Homo sapiens.

W09843436-A2.
15-OCT-1998: U06955.
10-APR-1997; US-838821.
(GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, M.
Racle LA, Spaulding V, Treacy M;
WPI; 99-070077/06.
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Best Loc
Matches
                                                                                                    Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou
                                                                                                                                                  15-FEB-1999
EST clone DA
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Sequence 592 BP; 197 A; 121 C; 105 G; 169 T;
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PS Claim 1; Page 288; 618pp; English.

CC The present sequence represents a human expressed sequence tag (EST).

CC The present sequence represents a human expressed sequence tag (EST).

CC The polynucleotide, which is a secreted EST, and the encoded protein conditions in human and animals although no supporting medical conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditivity, tissue growth activity, haematopoiesis regulating conditivity, tissue growth activity, activin/inhibin activity, constitution activity, tissue growth activity, haematopoiesis regulating condition to the polynucleotide may also be useful for gene therapy.

CC activity. The polynucleotide may also be useful for gene therapy.
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Best Local S
Matches 362
                                                   09-APR-1998.
03-CCT-1997; U18007.
04-CCT-1996; US-726237.
(GEMY) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie EF.
Racie LA, Spallding V, Treacy M;
WPI; 98-240082/21.
Nucleic acids encoding novel secreted anti-inflammatory, immuno-stimulatory Claim 45; Paye 80; 110pp; English.
                                                                                                                                                                                               Homo sapiens adult placenta clone DA136_11 5 cdult; placenta; cDNA library; clone DA136_1 therapeutic composition; autoimmune disease;
                                                                                                                                                                         suppression;
Homo sapiens.
                                                                                                                                                                                   therapeutic composition; suppression; ds.
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Pred. No. 9.8e
0; Mismatches
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                                                                            Мссоу
               or suppre
               suppressing
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6_11; anti-i;
se; immune;
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  nutrition used as a
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Sequence 340 BP; 101 A; 73 C; 79 G; 85 T;
                                               Nucleic acids encoding novel secreted proteins - useful as, e.g. anti-inflammatory, immuno-stimulatory or suppressing agents Claim 45; Page 82; 110pp; English.

The sequence is that of an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or ameliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers tissues, molecular weight markers for gels, primers or probes, for the sequence of th
                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC.

Agostino MJ, Jacobs K, Lavallie ER, Mccoy JM, Merberg Racie LA, Spaulding V, Treacy M;
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03-OCT-1997; U18007.
04-OCT-1996; US-726237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
WO9814576-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suppression; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V11623;
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                                                                                                                                                                                                                                                                           98-240082/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens adult placenta clone DA136_11 3' region.
t; placenta; cDNA library; clone DA136_11; anti-i
apeutic composition; autoimmune disease; immune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gactgagcttcaatgcatttggcacaacctgagctacatg
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337; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAATCTGCTGT
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     for
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eight markers for gels, primers or probes, for
nitrogen or carbohydrate source. They can also be
or cell proliferation and differentiation activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 336.4;
Pred. No. 9.4e
0; Mismatches
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No. 9.
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les 3;
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mmune; stimulation;
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                       Claim 1; Page 1252; 2245pp; Japanese.

CA single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                         01-707-1995.
01-707-1994; J01916.
11-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                          Matsubara
WPI; 95-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systemic lugus erythematosus, to regulate haematopoiesis, for growth, as an activator or inhibitor, or as a chemotactic or chemokinetic, haemostatic and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitor agents.

Sequence 285 BP; 93 A; 36 C; 50 G; 98 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as immune stimulants or suppressors, e.g. fo
infections, for autoimmune diseases such as
systemic lupus crythematosus, to regulate ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fomo sapiens.
FO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene signature HUMGS04672
Gene signature; messenger RNA; r
human; cloning; mapping; non-bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3802
                                                                                                                                                                                                                                                                                       WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell typing; abnormal cell function; ss.
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different cell
265 BP; 56 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                           Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      messenger RNA; mRNA; mapping; non-biased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.6%;
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types.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA; relative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258.4; DB 1
No. 1.4e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library;
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as multiple sclerosis
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TANGE SON CONTRACTOR 
CC apoptosis protein (IAP), and can be used in the method of the invention. CC apoptosis protein (IAP), and can be used in the method of the invention. CC proliferative disease by treatment with a compound that inhibits CC compounds are used to treat proliferative diseases. Specially cancers of CC compounds are used to treat proliferative diseases, specially cancers of CC liver nasopharnyx, thyroid, central nervous system, prostate, colon, CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP coliferative diseases. Transgenic animals are used for testing the effects of antisense color, cresistance to chemotherapeutic agents and mutations in p53 (it is colorance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP coliferative possible coliforned are used for testing the effects of antisense coliforned by the colorance of the IAP or NAIP col
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Claim 13; Fig 2; 147pp; English.
This sequence encodes the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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13-FEB-1998; IB0781.
13-FEB-1997; US-800929.
(UYOT-) UNIV OTTAWA.
Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt
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P-PSDB; W69295.
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Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein; ss.
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54; Conservative
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/product= HIAP-1
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Pred. No. 1.7e-50;
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Query Match

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6.0%;

Score

239;

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Truncary syndrome PS Claim 19; Pages 51-67; 84pp; English.

CC This is the human SHOX gene sequence containing the PARI region. The gene CC region corresponding to short stature has been identified as a region of genes in this region have been identified as candidates for the short CC stature gene. These genes were designated SHOX (also referred to as CC three). The SHOX gene has two separate SHOX-like homeobox gene on chromosome CC (short.stature homeobox-containing) genes SHOX FT92, SHOXA, SHOXB, SHOX GC (and exons of the SHOX genes as shown in V3561) to V3561 and protein cC sequences of the human growth protein transcription factor SHOXA, SHOXB GC Turner's syndrome. The products can be used to develop agents for the cC treatment of short stature or other human growth disorders. The products can also be used for providing a mitogenic effect on cells, e.g. for the with disturbance in the bone calcium regulation.

SC Sequence 32367 BP; 7627 A; 8130 C; 8564 G; 8043 T;
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16-JAN-1997; EP-100583
01-OCT-1996; US-027633
(RAPP/) RAFFOLD-HOERBRAND G.
RAO E, Rappold-hoerbrand G;
API; 98-271719/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.68;
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                                                                                                                                                                                                                                                                                                                               New human growth genes - used and treatment of human growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SHOX (short stature homeobox containing gene) gene sequence Homeobox domain; human growth gene; growth regulation; growth defeturner's syndrome; short stature homeobox containing gene; SHOXa; SHOX; bone disease; osteoporosis; calcium regulation; short stature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
W09814568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription factor A; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 32367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                       to develop products for the diagnosis defects such as short stature, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                           WO9814568-A1.
09-APR-1998.
29-SEP-1997; E05355.
16-JAN-1997; EP-100583.
01-OCT-1996; US-027633.
(RAPP/) RAPPOLD-HOERBRAND G
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Disclosure; Pages 37-45; 84pp; English.

This is a preliminary nucleotide sequence of the SHOX gene. The gene region corresponding to short stature has been identified as a region approximately 500 kb in the PARI region of the X and Y chromosomes. The genes in this region have been identified as candidates for the short
                                                                              Rao E,
WPI; S
                                                                                                                                                                                                                                                                                                                                     misc_feature
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Key
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98-271719/24.
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Sequence: 15577 BP; 3692 A; 3875 C; 4196 G; 3629 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 5.9%;
Local Similarity 81.8%;
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Pred. No. 1.2e
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28-JUN-1990; 307091
28-JUN-1989; US-37267.
20 LEC-1989; US-452951
(SCHE) SCHERING CORP.
MOSMICH TR. MOOTE KW. BOI
771; 31-009290/02.
                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1991
pH15C insert
**Ammalian cytokine synthesis inhibitory factors - capable of inhibiting synthesis of cytokine(s) associated with delayed-type hypersensitivity and useful in treatment of e.g. leishmaniasis Disciosure; Fig. 4; 31pp; English.

The gene product may be used in treatment of diseases associated
                                                                                                                                                                                                                                                                                                                                                            Delayed type hypersensitivity; DTH; MHC-assoliated autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q10207 standard; cDNA; Q10207;
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RESULT
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Best Local S
Matches 276
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27-JUL-1993.
28-JUN-1989; 372667.
28-JUN-1989; US-372667.
20-DEC-1989; US-453951.
06-AUG-1990; US-546235.
20-JUL-1992; US-917806.
Genes and proteins encoding cytokine synthesis inhibitory factors—useful in treating diseases associated with cytokine imbalances, e.g. parasitic infections and auto-immune disorders Claim 1; Fig 4; 23pp; English.

A human T cell cDNA library was screened with probes based on the murine CSIF gene. Two clones carrying plasmids pH5C and pH15C were identified. (These two expression vectors are claimed). The CSIF polypeptide they encode inhibits synthesis of cytokines associated with delayed type hypersensitivity responses. CSIF (also called II-10) can be used to treat diseases associated with cytokine
                                                                                                                                                                       Bond
WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytokine synthesis inhibitory factor clone pH15C. Mammalian cytokine synthesis inhibitory factor; CSIF; interleukin IL-10; immune system imbalance; human T cell; Leischmaniasis; rheumatoid arthritis; systemic lupus erythematosus; thyroiditis; myasthenia gravis; insulin-dependent diabetes mellitus; ss.
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93-249726/31.
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276; Conser
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Pred. No. 8e
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8e-49;
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C: This is the human SHOX gene sequence containing the PAR1 region. The gene corresponding to show that has been identified as a region of approximately 500 kb in the PAR1 region of the X and Y chromosomes. Three cidents in this region have been identified as candidates for the short contained the part of the X and Y chromosomes. Three cidents in this region have been identified as candidates for the short contained the X and Y chromosome in this region have been identified as candidates for the short contained the X and Y chromosome contained the X and Y chromosome contained the ABC (SHOX-like homeobox gene on chromosome contained the X and SHOX and SHOX and SHOX The Specification provides sequences of SHOX (Short stature homeobox-containing) genes SHOX ET92, SHOXA, SHOXD, SHOYT cand exons of the SHOX genes as shown in V3561 to V3561 and protein containing the product shown which the genes can cause short stature, e.g. containing the products can be used to develop agents for the Turner's syndrome. The products can be used to develop agents. The products can be used to develop agents.
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Matches 276
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Human SHOX (short stature homeobox containing gene) ger
Homeobox domain; human growth gene; growth regulation;
turner's syndrome; short stature homeobox containing ge
SHOY; bone disease; osteoporosis; calcium regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1437
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                                                                                                                                                                                                                              Turner's syndrome
Claim 19; Pages 51-67;
                                                                                                                                                                                                                                                          New human growth genes and treatment of human
                                                                                                                                                                                                                                                                                                                                     16-JAN-1997;
01-OCT-1996;
                                                                                                                                                                                                                                                                                        (RAPP/) RAPPOLD-HOERBRANI
Rao E, Rappold-hoerbrand
WPI; 98-271719/24
                                                                                                                                                                                                                                                                                                                                                                                  09-AFR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                              transcription
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276; Conser
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nilarity 80.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            factor A;
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excessive production
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Pred. No. 8e-4
0; Mismatches
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367 C;
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a gravis and thyroiditis.
356 G; 432 T;
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                   09-APR-1998.
29-SEP-1997; E05355.
16-JAN-1997; EP-100583.
01-OCT-1996; US-027633.
01APP) RAPPOLD-HOEBBRAND G.
RAPD RAPPOLD-HOEBBRAND G.
WPI; 98-271719/24
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Sequence 32367 BP; 7627 A; 8130 C; 8564 G;
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Sequence 15577 BP; 3692 A; 3875 C; 4196 G; 3629 T;
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Disclosure; Pages 37-45; 84pp; Er
This is a proliminary nucleotide
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	Insert Length: 816 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 450. I Location/Qualifiers 1673 //Coganism="Homo sapiens" //db_xref="taxon:9606" //clone="fyAgGE:2103714" //clone_lib="NCI_CGAP_Brn23" //tissue_type="glioblastoma (pooled)"	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Emmail: Robert_Strausberg@nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. 1 Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., N. Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Ediptering by: Washington University Genome Second Clone distribution: NCI-CGAP clone distribution infound through the I.M.A.G.E. Consortium/LLNL at: WWW-bio.llnl.gov/bbrp/image/image.html	Homo Sapiens Lukaryota; Metazoa; Chordata; Craniata; Vertebrata Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 673) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap National Cancer Institute / National Institute of Disorders and Stroke, Brain Tumor Genome Anatomy F (CGAP/BTGAP), Tumor Gene Index Unpublished (1998) On Apr 7, 1998 this sequence version replaced gi:3	* % % % 1	ALIGNMENTS	44 11.1 448 45 AI342477 44 11.1 445 47 AIS33044 43 11.1 445 41 AID17354 43 11.1 443 49 AIG23147 43 11.1 444 63 AN006551 42 11.0 444 62 AI887698 6 10.9 444 62 AI887698 35 10.9 435 43 AI89262 31 10.8 433 34 AAA78701 51 10.8 431 34 AAA78704 6 10.7 436 41 AID56642 6 10.7 436 41 AID56642 6 10.7 437 438 AAA991974 6 10.6 437 42 AIR87177 6 10.6 437 42 AIR87177 6 10.6 437 43 AAA991976 6 10.5 420 45 AIR67605	2 454 51 AI744242 2 448 42 AI088738 2 448 48 AI559614 2 448 63 AI983370 2 452 63 AW008384 1 447 44 AIZ75445 1 448 44 AIZ91764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1156 ttccctccaattcctgatcctggcaagatttttaaagaaatgttttggagaccagaatgat 1215
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                                                                                                                                                                                                                                                                                                 313 GAGTCATTCTCATTGAATTATAAAAGCCAGCCATCAAACTAGGGGACAAAGCAAAAA 254
                                                                                                                                                                                                                                                                                                                                                             373 CTTTATGTTGAGTCGCGCACCGAAAAACTAAAATAATGGGCGCTTTGGAGAAGAGTGTG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 TTCCGTCCATTTCTGATCCGTGCCAGAATTATAAAAGAAATGGTTGGAGACCAAAATGAT 614
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                 ttaacagtc 1824
                                                                        aaatctgatatgtattgtttgggatcctattgaaccatgtttgtggctattaaaactctt 1819
TTGGCAGTC 5
                                                       AAATCTGATATGTATTGTTTGGGATCCTATTGAACCATGTTTGTGGCTATTAAAACTCTT
                                                                                                                  GGGTGCAAATGCTAATGTCAAACTTGAGTCACAAAGAACATGTAGAAAACAAAATGGATA 74
                                                                                                                                 gggtgcaaattgctaatgtcaaacttgagtcacaaagaacatgtagaaaacaaaatggata 1755
                                                                                                                                                                                                                                                                                                                 gagtcattctcattgaattataaaagccagcaggcttcaaactaggggacaaagcaaaaa 1575
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Pred. No. 5.5e-107;
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Best Local
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                                                                                                                acacataatgttttctacgtccaagaggctaaatgtgagaatccagaatttgagagaaat 903
agccaagaaatgagtataggtaagaagcgcaattccacactctacataaccatgttactc
                                                                   agaataagagtcaaaacaaataagttatgctatgaggatgacaaactctggagtaattgg
                                                                                                                                                                                     ACACATAATGTTTTCTACGTCAAAGAGGCTAAATGTGAGAATCCAGAATNTGAGAGAAAT
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                                                 AGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGG
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On Dec 20, 1995 th
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g5235122
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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Location/Qualifiers
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Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the apol of 5,000 clones made from the Si32376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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1) 496-1550
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/db_xref="taxon:9606"
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Mismatches 3;
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On May 18, 1995 this sequence version
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Promational Cancer Institute, Cancer Genome Anatomy Promational Cancer Institute, Cancer Genome Anatomy Promatical Cancer Institute, Cancer Genome Anatomy Promatical Cancer Institute, Cancer Genome Cancer Ca
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ng30a07.sl NCI_CGAP_Co3
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Location/Qualifiers
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue_Procurement: Elias Campo, M.D., Michael R.
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Seq primer: -40ml3 fwd. ET from Amersham
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/tissue_type="colon"
/lab_host="DH10B"
/lab_host="DH7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:936276"
                                                                                                                                                                 /clone_lib="NCI_CGAP_Co3"
/sex="pooled"
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g5594153
                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 627)
                                                                                                                                                                                                           AI888989 627 bp. mRNA EST 01-SEP-1999 wj16b01.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402953 3'sinilar to SW:II31_HUMAN P78552 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR ;, mRNA sequence.
     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.
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/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors
/lab_host="DH10B"
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                   TCTCTGTTGAAGACCTCTGCACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                          This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DRT2); Email s. wiemannddkfz- heidelberg.de; sequenced by Qiagen within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,
                                                                                                                                                                                                                                                                                                                                                         No sl sequence available.
This clone is available at the RZPD in Berl:
Please contact the RZPD: Ressourcenzentrum,
Berlin-Charlottenburg, GERMANY; Email: clon
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/clone_lib="564 (synonym: h
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
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148 c 154 g
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/db_xref="taxon:9606"
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round through the I.M.A.G.E. Consortium/LLNL at: www-bio:llnl.gov/bbrp/image/image.html
                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email. Robert_Strausberg@nih.gov
                                                                                                                                                                  On Jun
                                                                                                                                                                                                                                                                                                                  AI816791.1
                                                                                   Emmert-Buck, M.D., Ph.D.
                           CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCT-CGAP clone distribution
                                                                                               Pissue Procurement:
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                  Tumor Gene Index
Unpublished (1997)
                                                                                                                  Eukaryota; Metazoa;
Eutheria; Primates;
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                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute. Cancer Genome Anatomy
                                                                                                                                                           Homo sapiens
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5, 1998 this sequence version
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Christopher Moskaluk, M.D.,

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Location/Qualifiers
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/tissue_type="2 pooled tumo
/lab_host="DH10B"
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/clone="IMAGE:2404697"
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db_xref="taxon:9606"
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Pred. No. 3.3e-95;
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al Similarity 100.0%;
528; Conservation
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406976.
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INAGE:755037 5', mRNA sequence
AA411323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned in the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:755037"
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; Pred. No. 1.6e-88;
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National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 521)
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wm17d11.x1 NCI_CGAP_Ut4
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                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
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              þ
                          /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.48 kb. Life Technologies catalog # 11542-016"
                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21g; 56cM"
                                                                                                /tissue_type="serous papillary carcinoma, high
pooled tumors"
                                                                                                                                         /clone="
                                                                                                                            clone_lib="NCI_CGAP_Ut4"
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                                                                                 lab_host="DH10B"
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clone IMAGE:2436213 3',
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Query Match

13.0%;

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521;

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1. (bases 1 to 507)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washy-NCI human EST Project
Unpublished (1997)
On Nov 6, 1997 this sequence version replaced gi:932221.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 455.
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ab88g12.s1 Stratagene
IMAGE:854086 3', mRNA
                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
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                                                                   Email: est@watson.wustl.edu
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                                                                                                3', mRNA sequence
AI436787
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 504) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                        th82f08.x1 Soares_NhHMPu_S1 Homo sapiens
3', mRNA sequence.
                                           Homo sapiens
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/db_xref="taxon:9606"
/clone="IMAGE:854086"
/clone_lib="Stratagene lung
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100.0%;
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Pred. No. 1.2e-84;
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ttggtagtcttcaaccagggattgtttctgttttaacttcttataggaaagcttgagtaaa
                                                                                         cagttaagtttttcccttcatctgggcactgaagggatatgtgaaacaatgttaacattt 3911
                                                                                                                                                                                ttttttcctaacatácctaagcaaacccagtgtcaggatggtaattcttattctttcgtt 3851
                                                                                                                                                                                                                                                                          | tcccatcccctgtgggaaattagtaggctcatttactgttttaggtctagcctatgtgga
                                                                                                                                                                                                                                                                                                                                                                    cttcttttagcagtaaaatagctgagggaaaagggaagggaaaaggaagttatgggaatac 367:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acattgatgctgacagtcatgcagtctgggagtggggaagtgatcttttgttcccatcct 3611
                                                                                                                                                         TTTTTTCCTAACATACCTAAGCAAACCCAGTGTCAGGATGGTAATTCTTATTCTTTCGTT 145
                                                                                                                                                                                                                                                     TCCCATCCCCTGTGGGAAATTAGTAGGCCCATTTACTGTTTTAGGTCTAGCCTATGTGGA
                                                                                                                                                                                                                                                                                                                                          CTGTGGTGGTTGTGATCCCTA@GTCTTGGGAGCTCTTGGAGGTGTCTGTATCAGTGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. Insert Length: 1009 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 18, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/map="917812; 1; 858608; 902A12; 960E05; 1q31.3-1q32.1;
1q31.3-1q32.1; 1q31.3-1q32.1; 1q31.3-1q32.1"
/cione="IMAGE:2125191"
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(Pharmacia) with a modified polylinker; Site_1: Not
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/tissue_type="Pooled human me]
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                                                               1815 tttaacagtctgggctgggtccggtggctcacgcctgtaatccccagcaatttgggagtcc 1874
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gaggcgggcggatcactcgaggtcaggagttccagaccagcctgaccaaaatggtgaaac 1934
                                         TTTAACAGTCTGGGCTGGGTCCGGTGGCTCACGCCTGTAATCCCAGCAATTTGGGAGTCC 60
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                                                                                                                              499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone original clone citation: see original entry for original citation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ahl4e02.y5 Gessler Wilms tumor Homo s
IMAGE:1156634 5' similar to contains
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Location/Qualifiers
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                                                                                                                            Conservative
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                                                                                                                                                                                                                                             /note-"Vector: pSPORT1; Site_1: SalI; Site_2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dT selection. CDNA library preparation was with
the BRL/Life Tech. Superscript Plasmid system. An
oligo-dT NotI primer for first strand synthesis generated
gcggccgcc(t)n at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcgaccacgcgtcg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPORT1.
Library was constructed by Dr. Manfred Gessler."

46 a 118 c 124 g 111 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Gessler Wilms tumor"
/sex="pooled (6)"
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/db_xref="taxon:9606"
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                                                                                                                                             12.48;
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                                                                                                                          Score 499; DB 60;
Pred. No. 3.8e-83;
0; Mismatches 2;
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1 (bases 1 to 498)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, ; Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Mooro, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washy-Merck EST Project 1997
Unpublished (1997)
Un Sep. 12, 1996 this sequence version replaced gi:1289000.
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                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                          /organism="Homo sapiens"
/db_xref="GDB:5923646"
                 /clone_lib="Soares_testis_NHT"
                                       /db_xref="taxon:9606"
/clone="IMAGE:726735"
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495; Conserv
Eukaryota; Metazoa; Chordata; Craniata; Verte
Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                    IMAGE:1739756 3', mRNA
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed
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                                                                                                                                                                                                    sequence.
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                  tgtttaacttcttataggaaagcttgagtaaaataaatattgtctttttgtatgtca 3996
                                                                 CTGAAGGGATATGTGAAACAATGTTAACATTTTTGGTAGTCTTCAACCAGGGATTGTTTC
                                                                                                                                                   agtgtcaggatggtaattcttattctttcgttcagttaagttttttccctttcatctgggca
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TGTTTAACTTCTTATAGGAAAGCTTGAGTAAAATAATATTGTCTTTTTGTATGTCA
                                                                                                                                AGTGTCAGGÀTGGTAATTCTTATTCTTTCGTTCAGTTAAGTTTTTCCCTTCATCTGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
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/db_xref="taxon:9606"
/clone="IMAGE:1739756"
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AA071468/c
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JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                      Matches 500;
3551 aacattgatgctgacagtcatgcagtctgggagtggggaagtgatcttttgttcccatcc
                                                                                                                                  3492 catttttactgttatcctattta-gatggccatgaagaggatgctgtgaaattcccaaca 3550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov)
Insert Length: 617 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 424.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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97044478
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AA071468.1 GI:1578899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA071468
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                                                                                                                                                                                                                                                                                                                                                                                                                                       174
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/clone="IMAGE:366079"
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/db_xref="GDB:1282783"
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98.6%;
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1 (bases 1 to 485)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., W;lie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                     Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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IMAGE:755037 3', mRNA sequence.
AA411324
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/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/ncte="Organ: ovary; Vector: pT7T3D (Pha:
                                                                      /organism="Homo sapiens"
/db_xref="taxon:9605"
/clone="IMAGE:755037"
/clone_lib="Soares ovary
                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                               1996 this sequence version replaced gi:1406977
                                                                                                                                                                                                                                                                                                        School of Medicine way, Box 8501, St. )
                                                                          tumor NbHOT"
                                                                                                                                                                                                                                                                                                          Louis,
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     (Pharmacia) with
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ORIGIN
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CACAAAGAACATGTAGAAAAACAAAATGGATAAAATCTGATATGTATTGTTTTGGGA 11
                   cacaaagaacatgtagaaaacaaaatggataaaatctgatatgtattgtttggga 1779
                                                                                                                         aacaaattttatttgtaggggaactcatttggggtgcaaatgctaatgtcaaactttgagt 1724
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M.Fatima Bonaldo. "
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Search completed: January 20, 2000, 05:25:49
Job time: 6362 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

January 19, 2000, 17:31:45; search time 34.07 Seconds (without alignments) 264.183 Million cell updates/sec

US-09-077-817-2 2104

Title: Perfect score: Sequence:

1 MAFVCLAIGCLYTFLISTTF.....LLLRKPNTYPKMIPEFFCDT 380

Searched: 188963 segs, 23686106 residues Scoring table:

BLOSUM62

Database : A_Geneseq_36:*

Word size :

0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match 100.0%; Score 2104; DB 1; Length 380; 3ϵ ; Tocal Similarity 100.0%; Pred. No. 8.1e-194; Mu whes 380; Conservative 0; Mismatches 0; Indels 0

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R78616	R78610	R20932	W56257	R92529	R78608
Expression vector	Expression vector	Sequence of beta-c	Interleukin-13 bin	Fas sequence from	Murine IL-3 recept

ALIGNMENTS

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expression of IL-13, its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours. Sequence $370~\text{AA}$:	in vivo, to > cell expressing at least one chain of the IL-13 receptor other than IL-13bc. IL-13bc can also be used in diagnosis to detect	activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied,	haematopoietic progenitor cells), cancer etc., and to increase macrophage	disorders, especially lupus, nephritis, thyroiditis and Grave's disease.	to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex	il-13bc proteins, and antibodies raised against them, are used to	mediator of the known biological activities of IL-13. Recombinant	The present sequence represents the human interleukin-13 (IL-13) binding	Claim 11; Pages 34-35; 49pp; English.	treating immunoglobulin E-mediated diseases, e.g. Graves disease,	for	New nucleic acid encoding interleukin-13 receptor binding chain and	11-12-13-13-13-13-13-13-13-13-13-13-13-13-13-		Collins M, Donaldson D, Fitz L, Neben T, Whitters M,	CLEAR LISSON US-6030/2./	28-FF3-1997; U03124.	04-SEP-1997	W09731346-A1./	Domain 363. 380	/1ab	/isber= extracer::tar_domain Domain 342362			Procein 26380	/label= signal_sequence /note= "putative"	Peptide 125		Fomo Serians	on; IgE-mediated cond	IL-13; interleukin-13 receptor	1998 (first entry)	W55295 standard; Protein; 380 AA. W35295;	,	1

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                        PT New nucleic acid encoding testis-specific cytokine receptor - useful PT for identification of ligands or antagonists, potentially for use as PT male contraceptives or for infertility treatment Claim 2; Page 47-48; 79pp; English.

CC This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and was isolated from human CC placental polya+ RNA. The resulting polyapeptide is a receptor for CC cytokines (particularly interleukin-13) and is expressed on the surface CC of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or CC differentiation of such cells in cultures and may also be used to treat CC ligand-receptor interactions and as male-specific contraceptives. By CC ligand-receptor can also be used to modulate immune function, e.g. in CC aligand and also to isolate and purify ligands. Antibodies can be used to cassay circulating receptor (an abnormal level may be indicative of CC disease such as cancer), for labelling cells that express the receptor, and the receptor, as antagonists.
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   Sequence
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L2-MAR-1997; U04043
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                                                                                                                                                                                                                                                                EP-812913-A2:
17-DEC-1997:
04-JUN-1997: 303815:
12-JUN-1996: US-017343:
(HUMA-) HUMAN GENOME SCI INC.
(SNIK ) SMITHKLINE BEECHAM COR
This protein comprises a novel human cytokine/peptide hormone receptors/designated HR-1 receptor. The amino acid sequence was deduced from a cDNA clone (see v04075) isolated from a human testis cDNA library. It shows 27% amino acid identity and 52% similarity with the human interleukin-5 receptor. Also claimed are polynucleotides encoding HR-1 receptor, vector and host cells, an agonist to the polypeptide, antibody against the polypeptide, an antagonist that inhibits the activity of the polypeptide, a process for diagnosing a disease, or a susceptibility to disease, related to expression of HR-1 receptor, and a method for identifying compounds that activate or inhibit the HR-1 receptor. HR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1998 (first entry)
Human cytokine/peptide receptor, HR-1 receptor.
HR-1 receptor; cytokine receptor; peptide hormone receptor; human; infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W41502 standard; Protein; 380 W41502;
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                                                                                                                                                              Claim 13; Page·27-28; 34pp; English.
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WPI; 98-034974/0
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Pred. No. 8.1e-194;
); Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                               Homo saplens HR-1 receptor.

Homo saplens HR-1 receptor; AIDS; acquired immune deficiency; Cytokine; hormone receptor; AIDS; acquired immune deficiency; syndrome; aplastic ansemia; neutropaenia; cancer treatment; syndrome; aplastic ansemia; neutropaenia; HR-1 receptor;
DNA encoding human cytokine-peptide hormone receptor treating preventing or diagnosing, e.g. lowered resis infection, asthma, allergy, or haematopoietic disease Claim 15; Fig 1; 75pp; English.

The sequence is that of the human cytokine/peptide ho:
                                                                                                                      09-JUL-1996; U11459.
12-JUN-1996; WO-U10262.
12-JUN-1996; WO-U17843.
(HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SWITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                      W33603 standard; Protein; W33603;
                                                                              N-PSDB; V02295
                                                                                            Appelbaum ER, Hu
WPI; 98-052309/05
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                                                                                                                                                                                                                                                Peptide
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invention relates to new purified peptides comprising 380 or 427 am acid sequences, which are receptors for interleukin-13 (II-13); the and 427 aa proteins are designated II-13R beta and alpha respective The II-13R beta has high affinity for II-13 while II-13R alpha has affinity, but acquire high affinity when associated with the II-4
                                                                                                                                                               SMEI ) SANOFI SA.

CEPUL D, FEITATA P, Laurent

PI; 97-319773/29.

N-PSIB: T85826, T86464.
                                                                                                                                 acids,
                                                                                                                                                                                                                                                                            Homo sapiens.
WO9720976-A1.
                                                                                       This
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97-NOV-1996; F01756.
%6-DFC-1995; FR-014424
                                                                                                                                                                                                                                                                                                                               Human interleukin-13 beta
                                                                                                                                                                                                                                                                                                                                                                           W24972
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                                                                                                                                                                                                                                                                                                                                          22-JUN-1995
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                                                                                                    laim 1; Figure 2a; 83pp; French
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                                                                                                                                 purified human interleukin-13 receptors is, useful for diagnosis and treatment of
                                                    sequence represents interleukin-13 (IL-13) beta receptor. The ntion relates to new purified peptides comprising 380 or 427 ami sequences, which are receptors for interleukin-13 (IL-13); the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRQ::CFVVRSKVNI:YCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
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3.1e-194;
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    and related
inflammation,

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                       18-DEC-1997.
12-JUN-1996; WO-U10262.
12-JUN-1996; WO-U10262.
(HUMA-) HUMAN GENOME SCI-INC:
(SMIK ) SMITHKLINE BEECHAM COR
APPELDAUM ER, Hu J;
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diagnostic pr
such as loss
  Appelbaum ER, Hu
WPI; 98-052308/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such as loss of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant II-13R beta and alpha which can be used as II-13 antagonists, specifically to regulate II-13-induced responses for treatment of inflammation and allergy. II-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of II-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression
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disorder; tumour; therapy; diagnosis.
                                                                                                                                                                                                                          /label= Sig_peptide
22. .380
/label= Mat_protein
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This protein comprises a novel human cytokine/peptide hormone receptor, designated the HR-1 receptor, that shows 27% identity and 52% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a CDNA clone (see VQ1431) obtained from a channel form the expressed in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoletic disorders, e.g. where induced by AIDS, aplastic anaemia, neutropaenia or cytotoxic treatments for cancer. HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor levels, since overexpression may be diagnostic of tumours.
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Best Local
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                                                                                                                 Human Zcytor2 cytokine receptor protein.
Cytokine receptor; 'ligand binding; testicular cell;
infertility; antagonist; contraceptive; diagnostic;
                                                                                 Homo sapiens.
WO9733913-A1.
                                                                                                                                                                         W36614 standard; Protein; W36614; W36614; Girst entry;
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Nucleic acid sequence encoding human cytokine peptide hormone
                18-SEP-1997.
12-MAR-1997; U04043.
13-MAR-1996; US-013345.
(ZYMO ) ZYMOGENETICS II
Baumgartner JW, Farrah
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Pred. No. 8.1e-194;
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Claim 1; Page 51-53; 79pp; English.

This sequence represents a novel ligand-binding receptor, Zcytor2, which

c shares homology with cytokine receptors and was isolated from a human

testis cDNA library. The resulting polypeptide is a receptor for

cytokines (particularly interleukin-13) and is expressed on the surface

of testicular cells, probably being involved in spermatogenesis. It can

be used to detect ligands that promote proliferation and/or

differentiation of such cells in cultures and may also be used to treat

infertility. Antagonists of this receptor may be used to characterise

ligand-receptor interactions and as male-specific contraceptives. By

blocking the action of IL-13, receptor antagonists and ligand-binding

this receptor can also be used to modulate immune function, e.g. in

allergy and asthma, as a diagnostic to determine circulating levels of

ligand and also to isolate and purify ligands. Antibodies can be used to

assay circulating receptor (an abnormal level may be indicative of

and theraponitically as antagonist
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Best Local S
Matches 377
W09733913-A1.
18-SEP-1997.
12-MAR-1997; U04043
                                                                                                                                                                                                         Celebus macaque Zcytor2 protein.
Cytokine receptor; ligand binding; test
infertility; antagonist; contraceptive;
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New nucleic acid en
for identification
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/note- "
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Pred. No. 2.5e
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No. 2.5e-191;
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tive; diagnostic;
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therapeutic.
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Best Local S
Matches 343
Homo sapiens.
WO9810539-A1.
19-MAP-1993.
                                                              Construct con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spermattogenesis. It can be used to detect ligands promoting proliferat and/or differentiation of such cells in cultures and may also be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of II-13, receptor antagonists ligand-binding this receptor can also be used to modulate immune function, s.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal leve may be indicative of disease such as cancer), for labelling cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and is isolated from testis tissue obtained from a Celebus macaque. The resulting polypept is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved
                                                                                                  W56260 standard; Protein; W56250; first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding testis-specific cytokine receptor - usef for identification of ligands or antagonists, potentially for use male contraceptives or for infertility treatment example 4; Page 56-57; 79pp; English.
                                                   autoimmune disease;
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(ZYMO) ZYM SENETICS INC.
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                                                               containing mature interleukin-13 binding ic; IL-3 mediated condition; allergy; asther.
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Pred. No. 9.26
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PR 10-SEB-1996; AU-002562.

A (AMRA-) AMRAD OPERATIONS PTY LT

I Hilton DJ, Nicola NA, Simpson R,

WPI; 98-207062/18.

N-PSDB; V22701.
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Best I
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27-FEB-1997; AU-005374.
10-SEP-1996; AU-002262.
(AMRA-) AMRAD OPERATIONS PHilton DJ, Nicola NA, Simp WPI: 98-207062/18.
N-PSDB; V22702.
   Disclosure;
The IL-13 bi
         New isolated interleukin-13 binding protein - used products for therapy e.g. for allergic conditions s for diagnosis or detection Disclosure; Page 55-56; 69pp; English.
                                                                                                                                                w56261;
16-SEP-1998 (first entry)
Mature interleukin-13 binding protein.
Mature interleukin-13 binding protein.
Mature interleukin-13 mediated condition; allergy; asthma; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma of the diagnosis or detection

Example 14; Page 52-53; 69pp; English.

The IL-13 binding protein and related therapeutic molecules can be in the antagonism of at least one IL-13 activity. They can be used treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after treatment. The products can also be used as diagnostic agents, edetecting autoimmune diseases. The antibodies can also be used fundamenterapy and may also be used as a diagnostic tool.
                                                                                                                                                                                                                             W56261 standard;
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Pred. No. 3.4e-160;
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                                                                                                                                                                                              04-SEP-1997.
28-FEB-1997;
01-MAR-1996;
                                 New nucleic acid encoding transformed cells - protei
                                                                                    N-PSDB;
                                                                                                                                                       Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine IL-13 binding chain of the IL-13 receptor. Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc; mediator; IL-13 receptor binding inhibition; IgB-mediated condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W35294;
                                                                                                                                                                             (GEMY)
                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the antagonism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as cartain allergic conditions such as astima or to inactivate locally administered IL-13 after IL-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool. Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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: Local Similarity
:hes 315; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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97-448632/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                    T75213
                                                                                                                                                     M, Donaldson D,
                                                                                                                                                                           GENETICS INST 1
              immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%;
ilarity 100.0%;
Conservative
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/note= "putative"
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                                      proteins,
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                                                                                                                                                   INC.
D, Fitz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343
       ng interleukin-13 receptor binding chain teins, antibodies and inhibitors, for E-mediated diseases, e.g. Graves disease
                                                                                                                                                                                                                                                                                          intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complex disorder.
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Pred. No. 2.8e-160;
0; Mismatches 0;
                                                                                                                                                     Neben
                                                                                                                                                Ŧ,
                                                                                                                                                   Whitters
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                                                                                                                                                                                                                                                                                                                                    RESULT 12
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CC The present sequence represents the murine interleukin-13 (IL-13) binding CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a CC mediator of the known biological activities of IL-13. Recombinant CC IL-13bc proteins, and antibodies raised against them, are used to combinate the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease. CC They are also used to treat immune deficiency (particularly in CC haematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein CC with such activity is combined with IL-13bc and the mixture applied, CC in vivo, to a cell expressing at least one chain of the IL-13 receptor CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect CC expression of IL-13, its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                              16-SEP-1998 (first entry)
Interleukin-13 binding protein N-terminal ORF J
Therapeutic; IL-3 mediated condition; allergy;
               Misc_difference
                                                                                                                                                                                                                                                                                    W56252 standard; Protein; 157 W56252;
                                                                                                                                 Misc_difference
                                                                                  Misc_difference
                                                                                                                                                                  Misc_difference
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                    354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALQCVDYIKADGONIGCREPYLEASDYKDEYICVNGSSENKPIRSSYFTEQLQNIVKPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSWARTTYWISPQGIPETKVQDMDCYYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLDWQCTNGSEVQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAFVCLAIGCLYTFLISTIFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
                                                                                                                                                                                                                                                                                                                                                                                    LIVEKEEPEPTL 365
                                                                                                                                                                                                                                                                                                                                                                                                                   LLLRKPNTYPKM 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEDICFFVRCKVNIYCADDGIWSEWSEEECWEGYTGPDSKII-FIVPVCLFFIFLLLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TROLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPWIEASYGISDEGSLETKIQDMKCIYYNWQYLVCSWKPGKTVYSDTNYTMFFWYEGLDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNKGIEGKIRTHLSEHCTNGSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAFY -- HIRCLCFILLCTITGYS ---- LEIKVNPPQDFEILDPGLLGYLYLQWKPPVVIE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                 /note= "Encoded by
                                                                                                                                        /note= "Stop codon"
                                                                                                                                                                                Location/Qualifiers
/label= Unknown
                                  note-
                                                                 note-
                                                                                                                 /label- Unknown
                                                                                                                                                                                                                antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.8%; Score 1194.5; DB 1; 58.9%; Pred. No. 1.3e-106;
                                  "Putative signal
                                                                 "Stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                immunotherapy
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                                                                                                  gtn"
                                  sequence"
                                                                                                                                                                                                                                   asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                   diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Fest Local
            involving IL-5
Chaim 21; Page 42-44; 65pp; English.
Chaim 21; Page 42-44; 65pp; English.
The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (IL-5) receptor, which is synthesised from murine early P cell mRNA; an isolated murine (secretory) IL-5 receptor; an isolated cDNA sequence encoding human (secretory) IL-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) IL-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a contg. The DNA; secretory human IL-5 lacking a cytoplasmic and a contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection.

Claim 7: Page 44: 69pp: English.

The IL-13 binding protein and related therapeutic molecules can be used in the antaconism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as certain allergic conditions such as astima or to inactivate locally administered IL-13 after IL-13 treatment. The products can also be used as diagnostic agents, e.g. fo detecting auroimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.

Sequence .57 AA;
11-5EP-1991; 308309.
17-5EP-1990; JP-240638.
(TAKA:/) TAKATSU K.
Takatsu K. Tominaga A. Takagi S. Murata
WPI, 92-090329/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of human interleukin 5 receptor with signal peptide (from a patient of eosinophilia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-1936; AU-002262.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Hilton DJ, Nicola NA, Simpson RJ,
                                                                                                                                                                                                                           Human and murine interleukin-5 receptor and DNA encoding for treatment of auto-immune and eosinophilia conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R22216 standard; Protein;
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WPI; 98-207062/18.
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27-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                      F-MAR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 MAFVCIAIGCLYTFLISTTFGCTSSSSTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAEVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
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                                                                                                                                                                                                                                                                                                                                                                                                        disorder; therapy;
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77.2%;
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Pred. No. 2.4e-36;
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Best Local (

Similarity

14.8%; 26.6%;

Score 311.5; DB 1; Pred. No. 6.2e-22;

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                                                             Query Match
Best Local Similarity
Matches 100; Conserv
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                                                                                                                                              involving IL-5
Disclosure; Page 49; 65pp; English.
Disclosure; Page 49; 65pp; English.
The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (IL-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) IL-5 receptor; an isolated cDNA sequence encoding human (secretory) IL-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) IL-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a
                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1992.
11-SEP-1991; 308309.
11-SEP-1990; JP-240638.
(TAKAF) TAKATSU K.
Takatsu K, Tominaga A, Takagi S, Murata
WPI; 92-090329/12.
                                                                                                                                                                                                                                                                                                                       Human and murine interleukin-5 receptor and DNA encoding for treatment of auto-immune and eosinophilia conditions involving IL-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R22219 standard; Protein; 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autoimmune disorder; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1992
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                              DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKICHLWIKLFP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRKPNTYPKMIP 374
DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL-----VIFVTGLL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFNQLFALHAIDQINPPLNVTAEI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNIHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                              14.8%;
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                                                               69;
                                                             Score 311.5;
Pred. No. 6.8e
59; Mismatches
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                                                             e 311.5; DB 1;
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ismatches 156;
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                                                             Indels
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RESULT 15
R32/20
                                                                                                                                                               Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                Disclosure; Page 51; 65pp; English.

The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (IL-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) IL-5 receptor; an isolated cDNA sequence encoding human (secretory) IL-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) IL-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a transmembrane region; and an expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human and murine interleukin-5 for treatment of auto-immune ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takatsu K, Tominag
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Sequence of
                                                                                                                                                                                                                                                                     Sequence
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ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSVVNLTCT
                                        KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
                                                                                                                       DYEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
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                                                                                                                                                                                                                                                                     396 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal
                                                                                                                                                               69;
                                                                                                                                                                                Score 311.5; DB 1
Pred. No. 6.2e-22;

    -5 receptor and DNA encoding
and eosinophilia conditions

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                                                                                                                                                                                                   DB 1;
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362	363	309	309	250	249	190	192	136	147
362 CKICHLWIKLFP 373	363 LRKPNTYPKMIP 374	RAAVSSMCREAGLWSEWS-OPIYVGNDEHKPLREWFVIVIMATICFILLILSLI 361	309 RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLL 362	250 EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV 308	249 ESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTTLVTATVENETYTLKTTNETROLCEVV 308	190 LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI 249	192 -GQNIGCREPYLEASDYKDEYICVNGSSENKPIRSSYETFQLQNIVKPLPPVYLTETR 248	136 INTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTEECQEYSKDT 189	WYEGLDHA
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Search completed: January 19, 2000, 20:00:50 Job time: 8945 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2000, 13:58:11; Search time 71.05 Seconds (without alignments) 252.278 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-077-817-2
2104
1 MAFYCLAIGCLYTFLISTTF.....LLLRKPNTYPKMIPEFFCDT 380

Scoring table: BLOSUM62

Database : PIR_62:* Searched:

142080 segs, 47169319 residues

Word size : 0

Number of hits that pass the threshold :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 142080

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 recentor A; Molecular S21050; MUID:92121815
A;Molecular S21050
   interleukin-5 receptor precursor,
C;Species: Homo sapiens (man)
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A;Residues: 1-128,'I','130-396 <MUW>
A;Cross-references: EMBL:x61177; NID:g33839; PID:g33840
A;Cross-references: EMBL:x61177; NID:g33839; PID:g33840
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane
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F;345-565/Domain: transmembrane #status predicted <MMY>
A;345-565/Domain: transmembrane #status predicted <MAT>
A;345-365/Domain: transmembrane #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X61177; NID:g33839; A;Experimental source: clone lambda h5R.27
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Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Jun-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248
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Pred. No. 2.2e-17;
                                  soluble (clone lambda h5R.25)
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C; Date:
C; Access
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C;Keywords: alternative splicing; cytckine receptor; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-33/Product: interleukin-5 receptor #status predicted <MAT>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent)
A; Cross-references: GB:M75914; C; Keywords: cytokine receptor;
                                                 A; Molecule type: mRNA
A; Residues: 1-335 <TAV>
                                                                                                                A; Reference number: A40267; A; Accession: A40267
                                                                                                                                                                                    Cell 66, 1175-1184, 199
                                                                                                                                                                                                                                C; Accession: A40267
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                                                                                           A; Status: preliminary
                                                                                                                                                               A; Title: A human high affinity interleukin-5 receptor
                                                                                                                                                                                                           R; Mavernier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-128, 'I', 130-333 <MUW>
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A; Residues: 1-333 <MUR>
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                                                                                                                                                                                                                                                                                                    interleukin-5 receptor alpha chain precursor -
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Experimental source: clone lambda h5R.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GQNIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
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                                                                                                                                                                                                                                                                                                                                                                                                                  RAAVSSMCREAGLWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ES----KCVTILHKGFSASVRTILQ----NDHSLLASSWASAELH-APPGSPGTSVVNLTCT
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                                                                                                                                                                                                           R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.9%;
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                                                                                                                                          MUID: 92005669
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  NID:g186387; PID:g186388 transmembrane protein
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Pred. No. 5.1e-16;
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13.9%;

Score Pred.

292; No.

6.2e-16;

Length 335;

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C:Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-331/Product: prolactin receptor #status predicted <MAT>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;539-91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-831 <TAN>
A; Cross references: DDBJ:D13154; NID:g222848; PID:d1002939;
A; Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin
A;Reference number: JQ1655; MUID:93075121
A;Accession: JQ1655
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C; Species: Gallus gallus (chicken)
C; Date: 30-Sep-1993 #sequence_revision
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Best Local Similarity
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                                    LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR---EDDTTLVTATVEN 290
                                                                                                                                                                   QSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGL
                                                                                                                                                                                                                                              DHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEV 119
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DPPVNVTLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ 390
                                                                      EQVYECPDY-RTAGPN-SCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQP
                                                                                                          DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP
                                                                                                                                              WSEWSSERHILIPSGQSPPEKPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGE 272
                                                                                                                                                                                                                   DASSNHLYHYELRIKPEEKEEWETI----SVGVQTQCKINR-LNAGMRYVVQVRCTLDPGE 212
                                                                                                                                                                                                                                                                                           TTFNITVTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETKRSANIMYLWAKWSPPLLA 156
                                                                                                                                                                                                                                                                                                                                TTFGCTSSSDTEIKVN--PPQDFE---IVDPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
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                                                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 263; DB 2; 26.4%; Pred. No. 3.8e-13;
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intcrleukin-2 receptor gamma chain - human
() Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: (04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C; Accession: A42565; A46591; T54332
R; Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; M.
Stience 257, 379-382, 1992
A; Title: Cloning of the gamma chain of the human IL-2 receptor.
A; Reference number: A42565; MUID:92335883
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C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision
                                           A;Reference number:
Accession: A42565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D90205; C; Keywords: cytokine receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; filtle: Molecular cloning a A; Reference number: S12357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Takaki, S.; Tominaga,
EMBO J. 9, 4367-4374, 1
                      A Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-415 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                               SES KPNTYPKMIP
                                                                                                                                                                                                                                                                                                                                                                                                                        306 RAAVSSPCRMPGRWGEWS-QPIYVGKE--RKSLVE-WHLIVLPTAACFVLLIF--SLICR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 VLGVLSSLICLIMSWTMVLKGYRMITFMLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 VTPLHEGFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVTNLTCTTHTVVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 PPQDEEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKD
                                                                                                                                                                                                                                                                                                                                   VCHLWTRLFP
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    type: nucleic
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1990
    acid;
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protein
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prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: I50455
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J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor A;Reference number: A46591; MUID:93293887
A;Accession: A46591
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A;Note: defects are associated with an X-linked form of severe combined C;Superfamily: interleukin-2 receptor gamma chain C;Keywords: cytokine receptor; duplication; immunodeficiency; severe compared to the combined compared to the combined compared to the combined comb
                                                                                                                                        A; Status: preliminary; translated
                                                                                                                                                                                     A; Reference number: A; Accession: I50455
                                                                                                                                                                                                                         A; Title: Cloning, expression, and mutational analysis A; Reference number: I50455; MUID:94283267
                                                                                                                                                                                                                                                                                                                                                             R; Chen, X.; Horseman, N.D.
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A; Map position: Xq13.1-Xq13.1
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A;Cross-references: GDB:134807; OMIM:308380
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A; Cross-references:
A;Cross-references: EMBL:U07694; NID:g466381; PID:g466382
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A;Residues: 1-369 <RE2>
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A;Residues: 1-369 <RES>
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Best Local S
Matches 70
                                                          ;Molecule type: mRNA
;Residues: 1-830 <CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTFVVQLQDPRE--PRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGVGLNTTILT-----PNGNEDTTADEFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SW-----KPGIGVLLDTNYNLFYWYEGLDH--ALQCVDYIKADGQNIGCRFPYLEASDY 207
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                                                                                                                                                                                                                                                                                                                    269-276, 1994
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Pred. No. 3.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells
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                                                                                                                                                                                                                                                                       얁
                                                                                                                                                                                                                                                              the pigeon prolactin receptor.
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                                                                                                                                                 325
                                                                                                                                                                                       232
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                                                                                                                                                                                                                                                                                                   207
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                                   338 KKTLLREWLPFGFILILVIEV 358
                                                                                                                                                                                                                          267 LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVD
                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 TTFGCTSSSDTEIKVNPPQDFEIVDPGYLG------
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IKDMV-VWIIVGVLSSLICLV 456
                                                                                                            TATVENETYTLKTTNETROLCFVV----RSKVNIYCSDD--GIWSEWS-DKQCWEGEDLS
                                                                                                                                                 VTYIVQTDPPVNVTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA---
                                                                                                                                                                                       LQNIVKPLPPVYLTFTRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV
                                                                                                                                                                                                                                                  FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQ
                                                                                                                                                                                                                                                                                                                                                                              SPPPLADVTSNSHVYRYELRLKPEEKEEWETV---SVGVQTQYKVNR-LQAGVKYVVQVR
                                                                                                                                                                                                                                                                                                                                                                                                                  QPPLSLDHFKECTV-EYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ 112
                                                                                                                                                                                                                                                                                                   CVLDIGEWSEWSSERHIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTL
                                                                                                                                                                                                                                                                                                                                       CINGSEVQSSWAETTYWISPOG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDINYNL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTYNITVMAMNEIGSNSS-----DPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAKW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%;
Similarity 24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 216.5; DB 2
Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOTATA ---- ALALOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
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                                                                                                                                                                                                                                                                                                   266
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R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468,
A:Title: Characterization of cDNAs encoding of cReference number: A47514; MUID:93391374
R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.;
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 recept
                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-369 <CAO>
                                                                                                                                                                                A; Cross-references: A; Accession: A47514
                                                                                                                                                                                                                                                                                                                                                                                                                                       injée:leukin-2 receptor gamma chain precursor - mouse
C;species: Mus musculus (house mouse)
C;bate: 27-Feb-1997 #sequence_revision 27-Feb-1997 #:
C;Accession: I49280; A47514; JN0592; JN0775; S37582;
                                                                                                                                                                                                                                                                                                            Reference number: A47514; Accession: I49280
                                                                           Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
                                                                                                                                                           Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                    preliminary;
                                                                                                        1-369 <RE2>
                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                         EMBL: U21795; NID: g727349;
                                                                                                                                                                                                                                                                                    translated
                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                            27-Feb-1997 #text_change
N0775; S37582; I53398
                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                         PIDN: AAA64279.1;
                                                                                                                                                                                                                                                                                                                                                                 murine
                                                     Nakamura,
                                                                                                                                                                                                                                                                                                                                                                 interleukin
                                                     .×
                                                                                                                                                                                                         PID:g727350
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                                                                                                                                                                                                                                                                                                                                                                 receptor
                                                                                                                                                                                                                                                                                                                                                               (IL-2R)
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A; Molecule type: mRNA A; Residues: 1-369 < KO

1-369 <KOB>

submitted to the EMBL Data Library,

October 1993

PIDN:BAA02974.1;

PID:d1003480; PID:g43604

A;Cross-references: GB:D13821; NID:g436045;

A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 A;Reference number: JN0775; MUID:93366191 A;Accession: JN0775

A;Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:d1003265; R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.

PID: 9303

A; Residues: 1-369 < KUM>

303-304, 1993

A; Molecule type: mRNA

Status: nucleic acid sequence not shown

A; Reference number: JN0592; A; Accession: JN0592

MUID:93277575

chain:

Demonstration

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K; DISANTO, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; AVEUR. J. Immunol. 24, 3014-3018, 1994
A; Title: The murine interleukin-2 receptor gamma chain gene: A; Reference number: I53398; MUID:95104285
A; Accession: I53398
                                                                                            R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puch Genomics 23, 69-74, 1994
A;Title: II-2Rgamma gene microdeletion demonstrates A;Reference number: A55718; MUID:95130114
A;Accession: A55718
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A; Reference number:
A; Accession: S37582
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A; Residues: 1-373 <HEN>
A; Cross-references: GB:
C; Superfamily: interleu
                                                             A; Status: prelimi
A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: interleukin-2 stimulated growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: receptor for interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C;Complex: The high affinity receptor is a heterotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X75337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-350, 'S', 352-366, 'S', 368-369
                                                                                                                                                                                                                                   interleukin-2 receptor gamma chain precursor -
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: IL-2Rgamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references:
                                                                                 Status: preliminary
                                                                                                                                                                                                             Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: interleukin-2 receptor gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250
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                                                                                                                                                                                                                                                                                                                                                                                    284
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                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PETKVQDMDCVYYNWQYLLCSW----KPGIGVLLDTNYNLFYWYEGLDHAL--QCVDYIK 189
                                                                                                                                                                                                                                                                                                                                                                                                                              LLRKPNTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRSKVNIYCSDDGIWSEWSDKQCWEG----EDLSKKTLLRFWLPFGF---ILILVIFVTGL 361
                                                                                                                                                                                                                                                                                                                                                                                    LERMPPIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SESQLELRWK--SRHIKERCLQYLVQYRSNRDRSWTELIVNHEPRFSLPSVDELKRYTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVENE-TYTLKTTNETRQLCFV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEITSGCQIQKEDIQLYQTFVVQL--QDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTLPLPEVQCFVFNIEYMNCTWNSSSEPQA----TNLTLHYRYKVSDNNTFQECSHYLF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                 A55718
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  interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                         Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.;
GB:U04361; NID:g517411; rleukin-2 receptor gamma
                                                                                                                                                                                                                                 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                              370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of CD44-mediated cellular adhesion by the IL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, A.; MacDonald, H.R.; Avner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                 18-Aug-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212.5; DB 2
No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHI
PIDN:AAC48403.1; chain
                                                                                                                                                                                                                                                                           dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116;
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                                                                                                                                                   that canine X-linked severe
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                   PID:g517412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.;
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                                                                                                                                                                                                                                                                                                                                               G:Superfamily: interleukin-3 receptor beta chain; cytokine r (Keywords: cytokine receptor; gupilcation; transmembrane pr F;1-22/Domain: signal sequence #status predicted <SIG> F:23+878/Product: interleukin-3 receptor beta chain #status
                                                                                                                                                                                                                                                                                                                                                                                                                                          A://olecule type: mRNA
A://rossidues: 1-815,'Q',817-878 <GOR>
A://ross-references: GB:M29855; NID:g198342; PIDN:AAA39295.1; PID:g309406
C:/Comment: In mice there are two classes of high-affinity IL-3 receptors.
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                                                                                                                                                                                                                                                                                                            F:39-236/Domain: extracellular #status predicted <EXT> F:39-236/Domain: cytokine receptor homology <CRS1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: A40091; A4302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Date: 30-Jun-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Gorman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AtStatus: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Figure: Cioning of an interleukin-3 receptor A; Figure on unber: A40091; MUID: 90117145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Mclecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; accession: A40091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin-3 receptor beta chain precursor
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       194 -TSNFQVN--LEPKL--FLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQPG-DKA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 NGNEDITPDFFLTATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSSEPRP--
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                                             YKDCFDLNKGIEAKIHTLLP-----
                                                                               PPKDIHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH
                                                                                                                    PPODFEIVDPGYLGYLYLOWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PRRQSTQKLKLQNLVIPWAPENLTLHNLSESQLELSWS---NRHLDHCLEHVVQYRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DTTLYTATYEN-ETYTLKTTNETROLCEVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLS
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                                                                                                                                                            59;
                                                                                                                                                        Score 195; DB 1; Length 878; Pred. No. 1e-07; Mismatches 150; Indels
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Pred. No. 3.
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                                           -WQCTNGSEVQ---SSWAFTTYWISPQGIPET 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-Jun-1993 #text_change
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RESULT 12
A39255
Cytokine receptor common beta chain precursor - human
C;Species: Homo sapiens (man)
C;Species: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
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F;461-897/Domain:
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C; Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology C; Superfamily: interleukin-3 receptor beta chain; cytokine receptor; duplication; transmembra C; Reywords: alternative splicing; cytokine receptor; duplication; transmembra F; 17-69 Domain: signal sequence #status predicted <SIG>F; 17-69 T; Product: cytokine receptor common beta chain #status predicted <MATY F; 17-43 J; Domain: extracellular #status predicted <EXTY>F; 35-232 J; Domain: cytokine receptor homology <CRS1>F; 35-232 J; Domain: cytokine receptor homology <CRS1>
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R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Title: Molecular cloning of a second subunit of the receptor A;Reference number: A39255; MUID:91088571
A;Accession: A39255
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A; Residues: 1-897 <HAY>
A; Cross-references: GB:M38275
C; Comment: The human high-affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB:CSF2RB
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 VNPPQDFEIVDPGYLGY------LYLQWQPP-----LSLDHF-----
                  IREDDTTLVTAT-VENETYTLKTTN----
                                                                                                                                                                                                                                                                                          VLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIG-----CRFPYLEASDYKDFYICVN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                    KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPQSHWLSPGDLEFEVYYKRL-QDSWEDAAILLSNTS-----QATLGPEHLMPSSTYVA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIPCQSFVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRVKPISDY---DGIWSEWSNEYTWT-TDWVMPTL---WI----VLILVFLIFTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRSK-VNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSLHWETQKIP---KYIDHTFQVQYKKKSESWKDSKTENLGRVNSMDLPQLEPDTSYCAR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKLKWSIPLGPIPARCFD--YEIEIREDDTTLVTATVEN----ETYTLKTTNETRQLCEV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY-LTFTRESSCE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPQNLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPAAPEEKCSPVVKEPQASVYTR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNI---
                                                                                                                                                    GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIE 275
                                                                                                                                                                                                                         VASSVSFGLFYKPSPDAGEEECSPVLR---EGLGSLHTRHHCQIPVPDPATHGQYIVSVQ 324
                                                                                                                                                                                                                                                                                                                                                                   RVRTRLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLECFFDGAAVLSCSWEVRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRCSLPVPEPSAHSQYTVSVKHLEQGKFI-MSYYHIQME----PPILNQTKNRDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KECTVEYELKYRNIGSETWK--TIITKNLHYKDGFDLNKGIE------A 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status predicted intracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%;
                                                                                   NI--QMAPPSLNVTKDGD-SYSLRWETMKMRYEHIDHTFEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 180.5;
Pred. No. 1.5e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-5,
              -ETRQLCFV-VRSKVNIYCSDDGIWSE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GM-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for human granulocyte-mac
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                                                                                   375
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                                                                                                                                                                                                                                                                                                                                                               267
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cytokine receptor common beta chain precursor cyspecies: Mus musculus (house mouse) cyspecies: 0.0-un-1993 #sequence_revision 30-Jun-C;accession: A35782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: rIL-3Rbeta
C;Superfamily: interleukin-3 receptor beta chain;
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Rattus sp
C;Date: 26-Jul-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-896 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: I56563; MUID:95370942
A;A:cession: I56563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Cloning of rat interleukin-3 receptor beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Neurosci. 15, 5800-5809,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Appel, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: I56563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.5%;
Best Local Similarity 21.4%;
Matches 87; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39-235/Domain: cytokine receptor homology . 253-433/Domain: cytokine receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 YKKD----TATWKDSKTETLQNAHSMALPALEPSTRYWARVRVRTSRTGY--
                                                                                                                                                                422
                                                                                                                                                                                                                                                                                                                                                                                                                                     155
                                                                                                                                                                                                                                         366 MSYPFIQHAFQVQYKKKLDRWEDSKT----ENLNHAHSMDLPQLEPGTSYCARVRVKTIP
                                                                                                                                                                                                                                                                                                                                                                                                 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TLLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 LFLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHWDSPTE-DKARPQNLQCFFDGIQSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 YLOWOPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIH 106
                                                                                                     14
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                                                                                                                                                                                                                                                                                                                                              NGSSENKPIRSSYFTFQLQ------NIVKPLPP-VYLTFTRESSCEIKLKWSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSEARSWDTESV---
                                                                                                                                                              EYKGLWSEWSNECTWT-TDWVMPTL---WI----VLILVFLILTFLL
                                                                                                                                                                                                SDDGIWSEWSDKOCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
                                                                                                                                                                                                                                                                             GPIPARCEDYEIEIR-----EDDTTLVTATVENETYTLKTTNETRQLCEVVRSKVNIYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVPRRCVLPYTQFSVSKEDYYSLQPDRDLSIHLVVPLAQHVQPPPPKDISISPSG--DHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLAIGCL--YT-FLISTTFGCTSSSDTEIKVN------PPQDFEIVDPGYLGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
                                                                                                                                                                                                                                                                                                                    NVSU----PAAHSQYTVSVKRLEQGKFIESFNHIQMNPPTLNLTKNRDS----YSLHWETQK
                                                                                                                                                                                                                                                                                                                                                                                                 CSWEVWEKVIDSVSFGLFYSSSPKAGEKKCSPVVKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                   CSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGONIGCRFPYLEASDYKDFYICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor beta-subunit ttus sp. (rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp. (rat)
96 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:S79263; NID:g1086954; PIDN:AAB35068.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --WOCTNGSEVQ---SSWAETTYWISPOGIPETKVQDMDCVYYNWQYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sauter, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.3e-06; 5; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178; DB 2; Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gebicke-Haerter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / <CRS1>
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                                                                                                                                                                                                                                                                                                                                                                                               -----LQASRYTRYHCSL
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A; Titlé: Cloning and expression of a gene encoding

M.; Itoh, N.; Kitamura, T.; Schr. Acad. Sci. U.S.A. 87, 5459-5463,

Schreurs,

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interleukin 3 Yonehara,

receptor-like Yahara,

pro

30-Jun-1993 #text_change

22-Jun-1999

mouse

R;Gcrman, D.M.;

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                                                                                                                         A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin receptor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Bos primigenius taurus (cattle)
;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Feb-1997
Query Match
Best Local Similarity
Matches 63; Conser
                                                                                                                                                                          Cross-references:
                                                                                                                                                                                                                                                                                                           Scott, P.; Kessler, M.A.; Schuler, L.A.
11. Cell. Endocrinol. 89, 47-58, 1992
Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactions.
                                                                                                                                                   Genetics:
                                                                                                                                                                                                Residues:
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Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: A35782; MUID:90319131 Accession: A35782
                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDB.
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53-434/Domain: cytokine receptor homology <CRS2>
42-463/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 VNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYE 273
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Local Similarity 20.7%;
les 81; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V-----KHLEQGKFIMSYNHIQMEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ
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                                                                                                                                                                                                type: mRNA: 1-581 <SC
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  Conservative
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7.8%; Score 165; DB 2; 31.3%; Pred. No. 1.4e-05; ive 24; Mismatches 96
                                                                                                                                                                                                                                                                                         MUID:93246019
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Pred. No. 5.2e:
69; Mismatches
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199 GOKYLVQIRCKPDHGYWSEWS
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                                                                                                                                                                                             GCP.PXLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIK 255
                                                                          PELWIKWSPPTMTDVKSGWFIIQYEIRLKPEKAT---
                                                                                                                                                        SCYFGEKHTSIWKMYVITVNAINOMGISSSDPLYVHVTYIVEPEPPANLTLELKHPEDRK
  219
                                                                              --DWETHFTLKQTQLKIFNLYP 198
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Scarci completed: January 19, 2000, 14:58:48
Job time: 3637 sec

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沙海城東京

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2000, 06:18:23; Search time 35.05 Seconds (without alignments) 315.340 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-077-817-2 2104 1 MAEYCLAIGCLYTFLISTTF.....LLLRKPNTYPKMIPEFFCDT 380

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database : SwissProt_38:*

Word size :

0

Number of hits that pass the threshold : 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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LMBL; X55302, CAA64617.1; - EMBL; U70581, AAB17170.1; - EMBL; U70581, CAA70021.1; - EMBL; Y07763; CAA70021.1; - MIM; 309216; - PFAM; P570041; fn3; 1. PYOSITE: P590340; RECEPTOR_CYTOKINES_2; 1. PYOSITE: P590340; RECEPTOR_ALPHA-2 CHAIN. DISUAL 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN. DOMAIN 27 343 EXTRACELLULAR (POTENTIAL). DOMAIN 364 380 CYTOPLASMIC (POTENTIAL). DISULFID 145 155 BY SIMILARITY. DISULFID 184 197 BY SIMILARITY.	is SWISS-FROT entry is copyright. It is produced through a collaboration etween the Swiss institute of Bioinformatics and the EMBL outstation he European Bioinformatics institute. There are no restrictions on it se by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercian nitities requires a license agreement (See http://www.isb-sib.ch/announce r send an email to license@isb-sib.ch).	NON N.A. (NVIELLE S.; (MAR-1997) to the EM (ON: BINDS AS A MONOM (), SUT NOT TO IL-4 LULAR LOCATION: TYPE LECTY: CONTAINS 1 FIRE LECTY: CONTAINS TO THE	"Clening and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain."; J. Biol. Chem. 271:16921-16926(1996). [2] SEQUENCE FROM N.A. TISSUE-TESTIS; DONALDSON D.D., WHITTERS M.J., FITZ L., NEBEN T., FINNERTY H., HENDERSON S.L., O'HANA R.M. JR., TURNER K.J., WOOD C.R., COLLINS M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.	ILIJARA OR ILIJAR. HOMO SAPIENS (Human). Eukkelyoka: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. IISSUE=REMAL CELL CARCINOMA; WEDLINE; 96279273. CLEOT D., LAURENT P., KAGHAD M., LELIAS J.M., LEFORT S., VITA N., FERBARA D.	ULT 1 1.32_HUMAN STANDARD; PRT; 380 AA. 1.32_HUMAN STANDARD; PRT; 380 AA. (1.4627; 0.0667; 01-NOV-1.997 (Rel. 35, Created) 01-NOV-1.997 (Rel. 35, Last sequence update) 15_UUL-1.999 (Rel. 38, Last annotation update) 15_UUL-1.999 (Rel. 38, Last annotation update) 1NTEF_LEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 BINDING PROTEIN).

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RESULT 2
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Best Local Similarity
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Q01344;
Q1-JUL-1993
Q1-JUL-1993
Q1-NQV-1997
              TAVERNIER J., DEVOS R., FIERS W., PLAETINCK G.;
                                   SEQUENCE OF 1-335 FROM N.A. MEDLINE; 92005669.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Structure and sequence of the l
Genomics 13:1311-1313(1992).
                                                                                                                                                                      "SCOTT H.S., GUO X.H.,
"Structure and sequence
                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92372031.
                                                                Molecular basis of the membrane-anchored and two the human interleukin 5 receptor alpha subunit."; Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
                                                                                                                CAVERNIER J.,
                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92357767.
                                                                                                                                                                                                                                                                       ANTIGEN)
                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125
                                                                                                                                                                                                                                                             IL5RA OR IL5R.
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interleukin-5 receptor (IL5R) is composed
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Pred. No. 6.7
0; Mismatches
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                                                                                                                                                                  .J., MORRIS C.P.;
human alpha-L-iduronidase gene.
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                                                                                                                VERHEE
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5.7e-157;
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                       VAN
                                                                                      soluble isoforms
                                                                                                              FIERS
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                     DER HEYDEN J.,
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Best Local
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EMBL; M96651; AAA59151.1; -
EMBL; M75914; AAA36110.1; -
EMBL; A26249; CAA01793.1; -
EMBL; A26251; CAA01794.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
VARSPLIC
VARSPLIC
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CARBOHYD
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DOMAIN
CARBOHYD
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00241; PROSITE; PS00340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               мім; 147851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A40267; A40267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>-</del> - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an IL5-specific alpha chain for GM-CSF."; Cell 66:1175-1184(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT
                                                                                                                                                                                                                                             87
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DATABASE: NAME-PROW; NOTE-CD guide CDw125 entry; WWW-,"http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSE RECEP SUBCELLULAR LOCATION: TYPE I THE STRUCK TWO SOLUBLE ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLUBLE MEMBRANE-BOUND FORM EXIST DUE TO ALTERNATIVE SPLIC
LGRN1ACWEPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI 249
                                                                                                                                                                                                                            KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                             DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
                                                                                                                                                                                                                                                                                                                           DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT
                               -GQNIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYETEQLQNIVKPLPPVYLTETR
                                                                                              TMTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE----
                                                                                                                                                                                   ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT 135
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR_CYTOKINES_1; FALSE_NEG.
RECEPTOR_CYTOKINES_2; 1.
mbrane; Glycoprotein; Alternative splicing; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.

POTENTIAL.

NDE -> FSR (IN SOLUBLE ISOFORM S1)

MISSING (IN SOLUBLE ISOFORM S2).

N -> K (IN SOLUBLE ISOFORM S2).

MISSING (IN SOLUBLE ISOFORM S2).

MISSING (IN SOLUBLE ISOFORM S2).
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 310.5;
Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                    .6e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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TWO SOLUBLE FORMS AND
TWO SPLICING OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                              -ECQEYSKDT
                                                                                                                                                                                                                                                                                                                                                                           47;
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RESULT
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                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 96133964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                            <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."; Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
-1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY TOGETHER WITH IL-4R-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                    CARBOHYD
                                                                                                                                                                                                            MGD; MGI:1
                                                                                                                                                                                                                       EMBL; S80963; AAB50695.1; -.
                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
                                                                                                                   DOMAIN
                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HILTON D.J., ZHANG J.-G., METCALF D.,
                                                                                                                                           TRANSMEM
                                                                                                                                                        NIAMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILLSON T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
LL13RA1 OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362
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                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                     TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY). SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDN TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKUME RECEPTOR CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
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IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY
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364
424
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          POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                          BY SIMILARITY
                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
POTENTIAL
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                                                               POTENTIAL.
                                                                                       BY SIMILARITY
                                                                                                     POTENTIAL.
                                                                                                                 IG-LIKE C2-TYPE
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                                                                                                                                                                                             Immunoglobulin domain;
                                                                                                                                                                                                                                                                                  There are no restrictions ong as its content is in
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                                                                                                                                                                   RECEPTOR ALPHA-1
                                                                                                                 DOMAIN
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Mus.
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RESULT 4
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Best Local
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01-20V-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
LATEXLEUKIN-13 RECEPTOR ALPHA-1 CHAIN
                                                  MEDLINE;
                                                                                                                                                                                  TISSUE-B-CELL;
GAUCHAT J.F.M., SCHLAGENHAUF E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
receptor alpha
                                                                                                                                                     JEANNIN P., MOUNEFOY J.Y.;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      "Cloning of the human IL-13R alphal chain and reconstitution with the IL4R alpha of a functional IL-4/\pmL-13 receptor complex."; FEBS Lett. 401:163-166(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I131_HUMAN
                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                             MILOUX B., LAURENT
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL13PA1 OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                              ERRARA P
                cDNA cloning and characterization
                                    EONARD W J.;
                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               HEDLINE: 97165986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 IGCLYTFLIST-TFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLOHFKECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CWEGEDLSK-KILLREWLPFGFILILV1FVTGLLLR-KPNTYP-----KMIPEFFCD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDINYNLFYWYEGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIGKEONSTEYTTMLLTIPV-EVAVAVIILLEYLKRLKIIIEPPIPDPGKIEKEMEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EDITTL-----VTATVENETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPDPS-PIKHLLKNGALLVQWKNPQN-FRSRCLTYEVEVNNTQTDRHNILEVEEDKCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPL-PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSRQC-ENTYREGQHIACSFKLTKVEPSFEHQNVQIMVKDNAGK--IRPSCKIVSLTSYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HALQCVDYIKADGQNIGCPFPYLEAS---DYKDFYICVNGSSENKPIRSSYFTFQLQNIV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLVKKC--ISPPEGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLYYWYSSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRYFSHI DOQUKKIAPET-----HRKEELPLDEKICLQVGS----QCSANESEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEY-- -- ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCT-NGSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGELLVLLLWTATVGQVAAA-*-TEVQPPVTNLSVSVENLCTIIWTWSPPEGAS--PNCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                  "AYEBI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.2%;
                                                                                                                                     6
                                                OBIRI N.I.,
                                                                                                                                                                                                                                                                                                                             BONNIN O., LUPKER J., CAPUT D., VITA N.,
                                                                                                                                     the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW;
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Pred. No. 3.5e-16
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae;
                                                                                                                                                                     FENG N.P., MC, NOTARANGELO
                                                  PURI R.K., MODI W.S.,
              0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427
              the
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                human
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                                                                                                                                                                                       MOSER R.,
                                                                                                                                                                     L.D.,
                interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IL-13R-ALPHA-1) (IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 424
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                                                                                                                                                                                       YAMAGE
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                <u>μ</u>
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Best Local S
Matches 107
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EMBL; Y09328;
EMBL; U62858;
HSSP; P31785;
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol.
                                                                                                                                                                                                                                                                                                   CONFLICT
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00041; fn3; 1.
184 CVDYIKADGONIGCRFPYLEASD -- YKDFYICVNGSSENKPIRSSYFTFQLONIVKPLPP 241
                               115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eceptor;
                                                              125
                                                                                         83
                                                                                                                       70
                                                                                                                                                   10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILIJR-ALPHA, AND POSSIBLY OTHER COMPONENTS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: UBIQUITOUS, HIGHEST LEVELS IN HEART, LIVER,
SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
SIMILARITY: CONTAINS' I IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.

SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
                                                                                                                                                                             LYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEY- 70
                           EKC -- ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ 172
                                              ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ 18:
                                                                                      SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV 114
                                                                                                           ----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
                                                                                                                                                 LWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF 67
                                                                                                                                                                                                              107;
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                 134
173
37
61
105
138
138
157
235
295
293
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CAA71669.1; -.
; CAA70508.1; -.
; AAB37127.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271:29265-29270(1996)
BINDS IL-13 WITH A LOW
                                                                                                                                                                                                                                                                                       48759
                                                                                                                                                                                                                            14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Immunoglobulin domain; Signal POTENTIAL.
                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                              63;
                                                                                                                                                                                                            Score 295.5;
Pred. No. 5.5e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
                                                                                                                                                                                                                                                                                    -> I (IN REF. 3).
-> D (IN REF. 3).
88E33C57 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
                                                                                                                                                                                                           i.5e-16;
hes 169;
                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                        Length 427;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                            73;
                                                                                                                                                                                                           Gaps
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DOMAIN TRANSMEM DOMAIN CHAIN Receptor;

SIGNAL

Transmembrane;

Glycoprotein; Signal; Repeat.

23 831 438

· DOMAIN

FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.

CYTOPLASMIC POTENTIAL

(POTENTIAL).

EXTRACELLULAR (POTENTIAL) PROLACTIN RECEPTOR POTENTIAL

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CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD

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PRLR_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRLR_CHICK Q04594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                    -1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-:- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2. PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
                                                    HSSP; P16471; 1BP3.
PFAM; PF00041; fn3;
                                                                                                         EMBL; D13154;
                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                            use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. I
                                                                                                                                                                                                                                                                                                                                                                                               the cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-WHITE LEGHORN; TISSUE-KIDNEY; MEDLINE: 93075121.
                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                     TANAKA M., MAEDA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                  ANAKA M., MAEDA K., OKUBO T., NAKASHIMA
Double antenna structure of chicken proj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 TLLREWLPF------GFILILVIFVTGL--LLRKPNTYP-KMIPEFFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 HIKNLSTHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTATVENETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                PROLACTIN
                                                                                        JQ1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-ENIFREGOYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR
                                                                                      JQ1655.
                                                                                                           BAA02439.1;
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29, Last sequence update)
36, Last annotation update)
R PRECURSOR (PRL-R) (CPRLP).
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Best Local S
Matches 103
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SEQUENCE
                                                                                                                                                                               receptor.
                                                                                                                                                                                                                                                                                                         INTERLEUKIN-5 RECEPTOR ALPHA CHAIN IL5RA OR IL5R. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                   01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                     P21183;
01-MAY-1991 (Rel. 18, Created)
                        This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                       Molecular cloning and expression
                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                            EDLINE; 91092260.
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                                                                                                                                                                                                                       AKATSU K.;
                                                                                                                                                                                                                                                                                                                                                                                                     L5R_MOUSE
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European Bioinformatics Institute. The by non-profit institutions as long
                                                              SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
                                                                                                   SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CEF RECEPTORS SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOP!
                                                                                                                                                                   FUNCTION: THIS IS
                                                                                                                                                       BINDS TO IL-5
                                                                                        ON B-CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEGEI--LILVIEVTGLLLRKPNTYPKMIP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR----EDDTTLVTATVEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ET-YTLKTTNETROLCFVVRSKVNIYCSDD--GIWSEWSDKQCWE-GEDLSKKTLLRFWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQVYECPDY-RTAGPN-SCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DASSNHLYHYELRIKPEEKEEWETI---SVGVQTQCKINR-LNAGMRYVVQVRCTLDPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTFGCTSSSDTEIKVN--PPQDFE---IVDPG-----YLGYLYLQWQPPLSL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTFNITVTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETKRSANIMYLWAKWSPPLLA
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831 AA;
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Sciurognathi; Murid
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POTENTIAL.
POTENTIAL.
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Pred. No. 4.2e-13;
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                                                                                                                                                                                                        of the murine interleukin-5
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There are no
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                                                                                                                                                                                                                                                                                   Murinae;
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Mus.
            restrictions
                          a collaboration
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350
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VCHLWTRLFP
                           KPNTYPKMIP 374
                                                                                                                           .IPLGP1fARCFDYEIEIREDD#----
                                                                                                                                                                  TEINSKGEEQLAVIJINGSSKRAAIKPEDQLESPLAIDQVNPPRNVTVEIESN-SLYIQWE
                                                                                                                                                                                                                                                                                                      GFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:96558
                                                                                RSKYNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFW----LPFGFILILVIFVTGLLLR
                                                                                                           KPLSAFPDHCFNYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSIQ------V
                                                                                                                                                                                                                       HTHLRPYQVSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPR
                                                      RAAVSSPCRMPGRWGEWS-QPIYVGKE--RKSLVE-WHLIVLPTAACEVLLIE--SLICR
                                                                                                                                                                                          -YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWS
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369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             46989
                                                                                                                                                                                                                                                                                                                                                                                                   11.7%;
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Pred. No. 3.2e-12;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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RESILE 7

FILL PRIL MELGA STANDARD; PRT; 831 AA.

I.) O91094; O91091; O91092;

I.) 10-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DF PRIL RECEPTOR PRECURSOR (PPL-R) (TPRIR).

GN PRIL R.

OS Meleagris gallopavo (Common turkey).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;

CC Neognathae; Galliformes; Meleagrididae; Meleagris.

R. SEQUENCE FROM N.A.

R. SEQUENCE FROM N.A.

RC MEDLINE; 97057891.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PITTS G.R., YOU S.K., FOSTER D.N., EL HALAWANI M.E.; Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L76587; AAB01544.1; ...
EMBL; U22947; AAA75038.1; ...
EMBL; U22924; AAA75039.1; ...
HSSP; P16471; IBP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHOU J.F., ZADWORNY D., GUEMENE D., KUHNLEIN U.;
"Molecular cloning, tissue distribution, and expression of the
prolactin receptor during various reproductive states in Meleagris
gallopavo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
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             179
                                      213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
DHALQCVDYIKADGQNIGCREPYLEASDYKDEYICVNGSSENKPIRSSYETFQLQNIVKP
                                      WSEWSSERRILISGGLSPPEKPTITKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGE
                                                            QSSW-AETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDINYNLFYWYEGL 178
                                                                                        DASSNHLYHYELRLKPEEKEEWETV---PVGVQTQCKINR-LNAGMRYVVQVRCMLDPGE
                                                                                                                DHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEV 119
                                                                                                                                           TTYNITYTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETQRYANIMYLWAKWSPPLLA 156
                                                                                                                                                                     TTFGCTSSSDTEIKVN--PPQDFE---IVDPG-----YLGYLYLQWQPPLSL 59
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                                                                                                                                                                                               l Similarity
97; Conser
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439
450
250
123
123
326
326
326
315
315
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                                                                                                                                                                                                           11.3%;
26.1%;
                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                               53;
                                                                                                                                                                                              Score 238; DB 1; 1
Pred. No. 3.7e-11;
53; Mismatches 178;
                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                              POTENTIAL. FB715C98 CRC32;
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PROLACTIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE-III.
                                                                                                                                                                                                                        Length 831;
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                                                                                                                                                                                               44;
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P31785;
MEDLINE; 94090
NOGUCHI M., NZ
LEONARD W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel: 26, Created)
01-JUL-1993 (Rel: 26, Last sequence update)
15-DEC-1998 (Rel: 37, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN)
                                                                                                                                                                                                                               ARAI K.-I., SUGAMUKA A., "Sharing of the interleukin-2 (IL-2) receptor receptors for IL-2 and IL-4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND MEDLINE; 94004847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                         PUCK J.M., DESCHENES S.M., PORTER J.C., DUTRA A.S., BRO WILLARD H., HENTHORN P.S.;
"The interleukin-2 receptor gamma chain maps to Xq13.1 in X-linked severe combined immunodeficiency, SCIDX1.";
Hum. Mol. Genet. 2:1099-1104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOGUCHI M., ADELSTEIN S., CAO X., LEONARD W.J.; "Characterization of the human interleukin-2 re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93293887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAKESHITA T., ASAO H., OHTANI K., ISHII N MUNAKATA H., NAKAMURA M., SUGAMURA K.; "Cloning of the gamma chain of the human science 257:379-382(1992).
                                                                                                                                                                                                                                                                             KONDO M., TAKESHITA T., ISHII N., NAKAMURA M., ARAI K.-I., SUGAMURA K.;
                                                                                                                                                           RUSSELL S.M.,
                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Primates;
                              MEDLINE; 94090316.
                                                                             interleukin-4 receptor.";
Science 262:1880-1883(1993).
                                                                                                                                                LELAND P
                                                                                                                                                                            MEDLINE; 94090317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 DPPANVTLELKKPINRKPYLMLTWSPPPLADVRSGWLTLDYELRLKPEEGEEWETVFVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 LPPVYLTFTRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIR-EDDTTLVTATVEN
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                                                                                                                                EONARD W.J.
                                                                                                                                                                                                                                                                                                                            DENTIFICATION AS A IL-4R SUBUNIT
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                                                                                                   interleukin-2 receptor gamma chain: a
iterleukin-4 receptor.":
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                                                                                                                                                                                                                        262:1874-1877(1993)
                                                                                                                                            M., KKEGAN A.D., HARADA N. FRIEDMANN M.C., MIYAJIMA
                NAKAMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                  ۲.,
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                RUSSELL S.M.,
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                                                                                                                                                Α.,
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                                                                                                                                              NAKAMURA Y.,
                  ZIEGLER
                                                                                                                 functional
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                  S.F.,
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gamma-chain mutation causing
immunodeficiency.";
J. Clin. Invest. 95:895-899()
                                                                                                    immunodeficiency in the IL-2R gamma ci conformation polymorphism analysis."; Hum. Genet. 96:427-432(1995).
                                                                                                                                                                                                                                                                                                                                                 ISHII N., ASAO H., KIMURA Y., TAKE KONNO T., MAEDA M., UCHIYAMA T., S "Impairment of ligand binding and receptor gamma-chains in patients immunodeficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                      "Detection of three nonsense mutations and one
the interleukin-2 receptor gamma chain gene in
differently affect the mRNA processing.";
Genomics 21:291-293(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked severe combined immunodeficiency disease result in the loss of high-affinity IL-2 receptor binding.";
Eur. J. Immunol. 24:475-479(1994).
                                                                                                                                                                                              gene causing human
                                                                                                                                                                                                                                                                        chromosome-linked severe
                                                                                                                                                                                                                                                                                                             WARIANT XSCID ASN-39. MEDLINE; 95023932.
                                                                                                                                                CLARK P.A., LESTER T.,
                                                                                                                                                           WARIANT XSCID
MEDLINE; 9601:
                                                                                                                                                                                                                MEDLINE; 95397841.
PEPPER A.E., BUCKLEY R.H.,
                                                                                                                                                                                                                                                               cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Interleukin-2 receptor gamma interleukin-7 receptor."; Science 262:1877-1880(1993).
VARIANT XSCID GLN-271 MEDLINE; 95190013.
                                                                                                                                                                                     "Two mutational hotspots in the interleukingene causing human X-linked severe combined Am. J. Hum. Genet. 57:564-571(1995).
                                                                                                                                                                                                                                                                                          DE SAINT BASILE G.;
                                                                                                                                                                                                                                                                                                   DISANTO J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT XSCID
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                                                       Female germ line mosaicism as
                                                                PUCK J.M., PEPPER A.E.,
                                                                                   VARIANT XSCID
                                                                                                                               Screening for mutations causing X-linked
                                                                                                                                                                                                                                                                                 Defective human interleukin
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                                                                                                                                                                                                                                    'ARIANTS XSCID CYS-226 AND
                                                                                                                                                                                                                                                                                                                                               mmunodeficiency.
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                                                                                                                                                                                                                                                     roc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                      Immunol. 153:1310-1317(1994).
                                                                                                                                                         xSCID SER-183.
96013903.
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94375038.
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                                                                                                                                                                                                                                                                                                   RIEUX-LAUCAT F., DAUTRY-VARSAT A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAUTRY-VARSAT A.,
                                                                                  GLN-HIS-TRP INS-237.
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                             95:895-899(1995)
                                                                                                                                                                                                                                                     Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and interleukin-4 receptors studied by molecular
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                                                                                                                                                GENET S.,
                                                       BEDARD P.-M.,
cism as the or:
                                                                                                                                                                                                                                                                       combined
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                                              X-linked
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                                                                                                                                                                                                                                                                                 2 receptor
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                                                                                                                                                 JONES
                                                                                                                                                                                                                                                                       immunodeficiency
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                                              severe combined
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-2 receptor gamma chain
immunodeficiency.";
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-!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TO RX-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: BOTOMAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD132 entry;
WWWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".
-- DATABASE: NAME-FIL2RGbase; NOTE-X-linked SCID mutation database;
                                                                                                                                                                                                                                                EMBL;
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DENNEY R.W., DAVE S.K., BRO
"Missenic mutation in exon
                                                                                                                                                                                                                                                                                                                                                   EMBL; D11085;
                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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MULLER-FLECKENSTEIN
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                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
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MEDLINE; 97042245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHARFE N., SHAHAR M., ROIFMAN
"An interleukin-2 receptor gan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TERIALT XSCID CYS-222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-cell-negative severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               At pical X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE SZINT BASILE G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cliin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WWW-"http://www.nhgri.nih.gov/DIR/LGT/SCID/IL2RGbase.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on gamma chain mutation.";
Genet. 99:677-680(1997).
                                                                                                                                                                           A42565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                L12178; AAA59145.1;
L12176; AAA59145.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.M., CLARK P.A.,
                                                                                                                                                                                             L19546;
                              PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2; Transmembrane; Glycoprotein; $\foatin{a}$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .Tryost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINNON C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Invest. 100:3036-3043(1997)
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                                                                                                                                          26-JAN-95.
26-JAN-95.
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                                                                                                                                                                           A42565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAVE S.K., BROOKS E.G., GOLDMAN
                                                                                                                                                                                                                                                                                                                                    AAA59145.1;
                                                                                                                                                                                                                                                                                                                                                    BAA01857.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMON SUBUNIT
                                                                                       fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on: in exon 7 of the common gamma chain x-linked combined immunodeficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95:1169-1173(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIRKSEN U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency due to possible to defect in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce,
                                Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation with normal thymus
                                                   1.
FALSE_NEG
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N A.S.
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H., FISCHER
                                                                                                                                                                                                                                                                                                                                                                                                                                       its content
                                    Disease mutation;
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- outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
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PRLR_COLLI
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Matches
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01-NOV-1997
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                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, e
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U07694;
HSSP; P16471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                        DOMAIN
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Columba livia (Domestic pigeon).
Eukaryota; Metazoa; Chordata; Craniata;
Neognathae; Columbiformes; Columbidae; (
                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocrinology 135:269-276(1994).
-:- FUNCTION: THIS IS A RECEPTOR
                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                            PROSITE;
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HORSEMAN N.D.;
                                                                                                                                                                                                                                                                                                PS00340;
                                                                                                                                                                                                                                                                                                                               PS00241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94283267
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                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAA20646.1; -.
                                                                                                                                                                                                                                                                                                                                                           fn3; 4.
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                                                                                                                                                                                                                                                        RECEPTOR_CYTOKINES_1; 2.
RECEPTOR_CYTOKINES_2; 2.
mbrane; Glycoprotein; Signal; Repeat.
23
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122
122
429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mutational analysis of the pigeon prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.50
B; Mismatches
                     CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN
                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                       PROLACTIN RECEPTOR
                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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ches 121;
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TYPE-III
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437 IKDMV-VWIIVGVLSSLICLV 456
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                                                                                                                                                                                                                                                                                                                  Local.Similarity.
les 93; Conserv
                      KKTLLRFWLPFGFILILVIFV
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                                                             TATVENETYTLKTTNETRQLCFVV----RSKVNIYCSDD--GIWSEWS-DKQCWEGEDLS
                                                                                       TYTYIVQTDPPVNYTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA----
                                                                                                            LQNIVKPLPPVYLTETRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV
                                                                                                                                    LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYYD
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                                                                                                                                                                                                                                                                                           TTFGCTSSSDTEIKVNPPQDFEIVDPGYLG-----
                                            ----EEWETIFVGQQTHYKMFSLNPGKKYIVQIHCKPDHHGSWSEWSLEKYLQIPTDFR
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75
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                       358
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Pred. No. 1.7e-09;
3; Mismatches 174;
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5EFADD51 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
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STRAIN-CBA/CA;
MEDLINE; 933913
CAO X., KOZAK (
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01-FEB-1994 (Rel. 2
15-DEC-1998 (Rel. 3
CYTOKINE RECEPTOR (
                                                                                                demonstration of functional
                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 93277575.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                             P34902;
                                                                                                                                                                                                                                                                                                                           CYRG_MOUSE .
                                          SEQUENCE FROM N.A.
                                                                       Biochem.
                                                                                 receptors
                                                                                                             "Cloning of the mouse
                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                          (INTERLEUKIN-2 RECEPTOR
  ; 93391374.
KOZAK C.A.,
                                                                    Biophys.
                                                                                                                                                                                                                        L. 28, Createu,
1. 28, Last sequence update)
1. 37, Last annotation update,
1. 37, Last annotation update,
(OR COMMON GAMMA CHAIN PRECURSOR (
RECEPTOR GAMMA CHAIN) (IL-2R GAMM
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                     Res.
    LIU
                                                                                                                          TAKESHITA
                                                                                                             interleukin 2
                                                                     Commun.
 Y.J.,
                                                                                                 differences
 NOGUCHI M.,
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                    193:356-363(1993)
                                                                                  369
                                                                                                             H., NAKAMURA M., eptor gamma chain:
                                                                                                                                                                                                                                                                                                                             B
 O'CONNELL E., LEONARD
                                                                                                                                                                                                                                        SOR (GAMMA-C)
GAMMA CHAIN) (P64).
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                                                                                                  mouse
                                                                                                                             SUGAMURA
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EMBL: D13565;
EMBL: L20048;
EMBL: S75852;
EMBL: S75844;
EMBL: S75845;
EMBL: S75848;
EMBL: S75848;
EMBL: S75848;
EMBL: S75849;
EMBL: S75849;
EMBL: S75850;
EMBL: S75851;
DISULFID DISULFID
                      TRANSMEM
DOMAIN
DOMAIN
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"The murine interleukin-2 receptor gamma chain gene: chromosomal localization and expression in the adult Eur. J. Immunol. 24:3014-3018(1994).
                                                      CHAIN
DOMAIN
                                                                             Receptor;
                                                                                                                                                     PIR; JN0592; JN0592.
PIR; JN0775; JN0775.
                                                                                                                                                                                                                                                                                                     EMBL; D13821; EMBL; U21795;
                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL-2R gamma chain Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma.
                                                                                                                                             HSSP; P31785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOUGHERTY G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95104285
DISANTO J.P., CER
                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOBAYASHI N., NAKAGAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of cDNAs encoding the murine interleukin 2 receptor IL-2R) gamma chain: chromosomal mapping and tissue specificity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular mechanisms regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96341745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLY ALSO THE IL-13 RECEPTORS.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adhesion protein CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKINS.
                                                                                                                                MGI:96551;
                                                                                                                       PF00041;
                                                                                                   PS00340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROLL A., COOPER D.L.,
23
264
285
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102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE GAMMA CHAIN IS COMMON TO
                                                                                                                       l; IL2RG.
: fn3; 1.
                                                                                                                                                                                                                                    AAB32904.1;
AAB32904.1;
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                                                                                                                                                                                                                                                                                                                BAA02974.1;
                                                                                                                                                                                                                                                                                            BAA02760
                                                                                                                                                                                                                                                                                                      AAA64279.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.";
Sci. U.S.A. 90:8464-8468(1993)
                                                                                                 RECEPTOR_CYTOKINES_1; 1
RECEPTOR_CYTOKINES_2; F;
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BY SIMILARITY
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the cDNA e
                                                                                                 CYTOKINES_2; FALSE_NEG
         CYTOPLASMIC
FIBRONECTIN
POTENTIAL.
                                            POTENTIAL
                                                      EXTRACELLULAR (POTENTIAL)
                                                                 CYTOKINE RECEPTOR COMMON GAMMA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the hyaluronan binding activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOUGHERTY S.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding a mouse IL-2
                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                      Signal.
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                      TYPE-III
                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                           Usage
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
(INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
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CARBOHYD
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                                      between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                     This
                                                                                                                                                INTERLEGENOS.

1. SUBCELLULAR LOCATION: TYPE I MEMBRA

1. SUBCELLULAR LOCATION: TYPE I MEMBRA
                                                                                                                                                                                                                        Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                  "IL-2R gamma gene microdeletion demonstrates that canine X-linked severe combined immunodeficiency is a homologue of the human
                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Canis familiaris (Dog).
Craniata; Vertebrata;
Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                           "!- FUNCTION:
                                                                                                                                                                                                                                     disease.'
                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                           ELSBURG P.J.;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Sutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                       ISSUE-SPLEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 PETKVQDMDCVYYNWQYLLCSW----KPGIGVLLDTNYNLFYWYEGLDHAL--QCVDYIK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                          SEVERE COMBINED IMMUNODEFICIENCY.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                SUBSECTION TYPE I MEMBRANE PROTEIN DISEASE: DEFECTS IN 11226 ARE THE CAUSE OF A CREVEDE COMBINED TO THE CAUSE OF A CREVEDE COMBINED.
                                                     SWIJS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRSRYNPICGSSQQWSKWSQPVHWGSHTVEENPSLFALEAVLIPVGTMGLIITLIFVYCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRSKVNIYCSDDGIWSEWSDKQCWEG----EDLSKKTLLRFWLPFGF--ILILVIFVTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SESOLELRWK - - SKHIKERCLOYLVQYRSNRDRSWTELIVNHEPRFSLPSVDELKRYTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVENS TYTLKTTNETROLCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEITSGCQIQKEDIQLYQTFVVQL--QDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTLPLPEVQCFVFNIEYMNCTWNSSSEPQA----TNLTLHYRYKVSDNNTFQECSHYLF
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67: Conser
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                                                                                                                                                                                                                                                                                           SOMEERG R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                immunodeficiency
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                            institutions as long
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26.9%;
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                                                                                                                                                                                                                                                                                          FIMIANI V.M.,
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Pred. No. 1.3e-09;
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                                     There are no
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                            as its content
http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                        PUCK J.M., PATTERSON D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116;
           Usage
                                                                                                                                                                              IL-2,
                                                                                                                                       CANINE X-LINKED
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                                      ne EMBL outstation restrictions on it
              and for
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Query Match
Best Local Similarity
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                                                                                                                                                                                 IL3B_MOUSE STANDARD;
P20954;
O1-OCT-1993 (Rel. 27, Created)
O1-OCT-1993 (Rel. 27, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                  LT 12
MOUSE
                          SEQUENCE FROM N.A.
MEDLINE; 90117145.
IITOH N., YONEHARA S., SCHREURS J., GORMAN D.M., MARUYAMA K., ISHII
IYOH N., ARAI K., MIYAJIMA A.;
"Clonting of an interleukin-3 receptor gene: a member of a distinct
receptor gene family.";
Science 247:324-327(1990).
                                                                                                                                                            U1-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN
ALICA OR IL3RB2 OR IL3R.
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CARBOHYD
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                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                            Eutheria;
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  FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3 RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
                                                                                                                                                                                                                                                                                                                                                                                                               NKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
                                                                                                                                                                                                                                                                                                   KENPLFASEAVLIPLGSMGLIISLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGNEDITPDFFLTATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSSEPRP--
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                                                                                                                            Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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RECEPTOR_CYTOKINES_2; FALSE_NEG
                                                                                                                      Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 208; DB 1;
    Pred. No. 3e-09;
48; Mismatches 108
                                                                                                                                                                          nnotation update)
II BETA CHAIN PRECURSOR
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FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                        358
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                                                                           GORMAN D.M., MARUYAMA K., ISHII A.,
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15-JUL-1998
CYTOKINE REC
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RESULT 13
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SEQUENCE
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CYRG_BOVIN
Q95118;
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                                                                                                                                       308 VRSK-VHIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEAM; PF00041; fn3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entitles requires a license agreement (s
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                      248
                                                                                                      415 VRVKPISDY --- DGIWSEWSNEYTWT-TDWVMPTL---WI----VLILVFLIFTLLL
                                                                                                                                                                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 PPKDIHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH
                                                                                                                                                                         358 YSLHWETQKIP---KYIDHTFQVQYKKKSESWKDSKTENLGRVNSMDLPQLEPDTSYCAR 414
                                                                                                                                                                                                              254 IKLKWSIPLGPIPARCFD--YEIEIREDDTTLVTATVEN----ETYTLKTTNETRQLCFV 307
                                                                                                                                                                                                                                                                                                                                                     139 KVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNI----
                                                                                                                                                                                                                                                                                                                                                                                      194 -TSNFQVN--LEPKL--FLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQPG-DKA
                                                                                                                                                                                                                                                                                                                                                                                                                   91 YKDGFDLNKGIEAKIHTLLP*------WQCTNGSEVQ---SSWAETTYWISPQGIPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 PPQDFEIVDPGYLGYLYLQWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLH
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                                                                                                                                                                                                                                                                                                                  QPQNLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPAAPEEKCSPVVKEPQASVYTR
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il Similarity 24.1%;
.86; Conserva+***
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                  STANDARD;
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Pred. No. 8.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                  379
                  8
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                                                                                                                                                                                                                                                                                 253
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997 (Rel. 35, Last sequence update) 998 (Rel. 35, Last annotation update) RECEPTOR COMMON GAMMA CHAIN PRECURSOR

(GAMMA-C)

35; Created)

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Best Local :
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P31785; 1ILN.
PFAM; PF00041; fn3; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma gene.";
DNA Cell Biol. 15:453-459(1996):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U33748; AAB07812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 96268473.
                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
IL2RG.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIAMOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                       ARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             MAIN
                                                                       169
                                                                                                                             111
                                                                                                                                                                                                              135 IPETKVQDMDCVYYNWQYLLCSW------KPGIGVLLDTNYNLFYWY---EGLDHALQCV 185
              226 YTFRVRSRYNPLCGSAQHWSDWSYPIHW-GSNTSKENIENPENPSLFALEAVLIPLG 281
                                           304
                                                                                                                                                     186 DYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLF 245
                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBABLY ALSO THE IL-13 RECEPTORS
                                                                                                                          HYLFSEGITSGCWFGKKEIRLYETFVVQLQDPREHR--KQPKQMLKLQDLVIPWAPENLT
                                        LCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG 360
                                                                    LRNLSEFQLELSWS---NRYLDHCLEHLVQYRSDRDRSWTEQSVDHRHSFSLPSVDAQKL
                                                                                               FTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVEN-ETYTLKTTNETRQ 303
                                                                                                                                                                                  LPLPKVQ---CFVFNVEYMNCTWNSSSEPQP-----NLTLHYGYRNFNGDDKLQECG 110
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions we are by and it was and this statement is not removed. Usage by and it was and this statement is not removed. Usage by and it was and this statement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tran
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            smembrane;
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                                                                                                                                                                                                                                                       9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                       Score 189.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
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FIBRONECTIN
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                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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TYPE-III.
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                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                 Length 379;
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                                                                                                                                                                                                                                        27;
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63

--KECTVEYELKYRNIGSETWK--TIITKNLHYKDGFDLNKGIE---

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VNPPQDFEIVDPGYLGY---

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Query Match
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Matches 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.

-I STUBULT: HETERODIMER OF AN LILPA AND A BETA CHAIN. THE BETAGRITY: HETERODIMER OF AN LILPA AND A BETA CHAIN. THE BETCHAIN. IS COMMON TO THE II-5 AND GM-CSF RECEPTORS.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARLITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- SIMILARLITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-I- DATABASE: NAME-PROW; NOTE-CD guide CDw131 entry;
FWM-"http://www.ncbi.nlm.nih.gov/piow/cd/cdw1.31.htm".
                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration petween the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1905 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYRB_HUMAN STANDARD;
p32927;
u1-OCT-1993 (Rel. 27, Created)
01-FEB-1906 (Rel. 33, Last seg
01-NOV-1997 (Rel. 35, Last ann
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    andified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The surpease by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted (FEB-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte-macrophage colony-stimulating factor (GM-CSF): reconstitution of a high-affinity GM-CSF receptor."; Proc Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSF2FB OR ILSRB OR IL3RB.
                                                                                                                                                                                                                                  DOMAIŃ
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M59941; AAA18171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Frimates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KITAMUKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE: 91088571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                138981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A39255; A39255
                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00041; fn3; 2
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    PS00340;
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
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                                                                                                                                                                                                                                                                                                                  897
443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Mammalia;
                     8.5%;
                                                                                                       WW;
  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GORMAN D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                _CYTOKINES_2;
Score 178.5;
Pred. No. 1.7e
97; Mismatches
                                                                                                                             POTENTIAL
                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
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BY SIMILARITY.
                                                                                                                                              POTENTIAL.
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                                                                                                       AC43EA5E CRC32;
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                       1.7e-06;
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                                      Length 897;
  Indels
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  105;
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                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                 receptor gene family.";

proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).

-I- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERL AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.

-I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BET CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

-I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR
                   TRANSMEM
                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GORMAN D.M., ITOH N., KITAMURA T
YAHARA I., ARAI K., MIYAJIMA A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 90319131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                      CHAIN
                                                                                                                                                                                      EMBL; M34397; AAA37204.1; -.
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                                    MAIN
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like protein: identification of another member
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                                                                                                                                         PF00041; fn3;
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; Transmembrane; (1 2 2 2 8 9 6 2 3 4 4 1 4 4 2 4 6 3 4 6 4 8 9 6 ...)
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                                                                                                  RECEPTOR_CYTOKINES_1; 1. RECEPTOR_CYTOKINES_2; 1.
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                                                                  Glycoprotein;
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CYTOPLASMIC (POTENTIAL)
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K-TDWVMPTL---WI----VLILVFLILTLLL 461
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                        EGEPLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                VQYKKKSDSWEDSKTENLDRAHSMDLSQLEPDTSYCARVRVKPISNYDGIWSKWSEEYTW
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FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
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POTENTIAL.
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Pred. No. 4.3e-06;
9; Mismatches 185;
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AA906051 CRC32;
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Search completed: January 20, 2000, 06:19:55
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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01-NOV-1998 (TremBLrel. 08, L
01-NOV-1998 (TremBLrel. 08, L
IL-13 RECETTOR ALPHA 2.
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EJEBL U65747; AAC33240.1; -.
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"The murine IL-13 receptor alpha 2: molecular cloning chiracterization, and comparison with murine IL-13 rec
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DONALDSON D.D., WHITTERS M.J., FITZ J., NEBEN T.Y., HENDERSON S.L., O'HARA R.M. JR., BEIER D.R., TURNER
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
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Q92913 homo sapien
Q928733 oryctolagus
Q10466 homo sapien
O57520 xenopus lae
O46600 bos taurus
Q89000 vesicular s
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Q89064 vesicular s
O61210 caenorhabdi
Q27950 bos indicus
C002207 homo sapien
Q63257 rattus norv
Q88999 vesicular s
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Q88206 bos taurus
Q007784 gallus gall
Q62960 rattus norv
Q70535 rattus norv
Q97394 drosophila
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Number of hits that

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Database : Searched:

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Scoring table:

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Title: Perfect score:

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Best Local :
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Q14633;
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SEQUENCE
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MEDLINE; 92121815.
MURATA Y., TAKKKI S., MIGITA M., KIKUCHI Y., TO
"Molecular cloning and expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TremBLrel.
01-NOV-1998 (TremBLrel.
01-ERLEUKIN-5 RECEPTOR P
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3L; X61176; CAA43483.1; -.
  CKICHLWIKLFP
                                                LRKPNTYPKMIP
                                                                                                                                             RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL -----VIFVTGLL 362
                                                                                                                                                                                                                                          ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVV
                                                                                                                                                                                                                                                                                             LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
                                                                                                                                                                                                                                                                                                                                                                                               TNTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT
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                                                                                                 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
                                                                                                                                                                                              EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSVVNLTCT
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420 I
47670 MW;
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Pred. No. 7.9e-20;
69; Mismatches 156;
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INTERLEUKIN-5 RECEPTOR.
; 247AB980 CRC32;
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Best Local
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                                                Cavia porcellus (Guinea
Eukaryota, Metazoa, Chor
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
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01-NOV-1996 (TYEMBLEE]. 01, Last sequence up
01-NOV-1998 (TYEMBLEE]. 08, Last annotation
INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
                                        Eutheria;
                                                                                        INTERLEUKIN-5 RECEPTOR
   Norris
             SEQUENCE FROM N.A.
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MURDLINE; 92121815.
MURATA Y. TAKAKI S., MIGITA M., KIKUCHI
"Molecular cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                    CKICHLWIKLEP 373
                                                                                                                                                                                                                                                                                                                     EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
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                                                                                                                                                                                                                                                                    RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI 361
                                                                                                                                                                                                                                                                                             RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL-----VIFVTGLL
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x61177; CAA43484.1; -.
   T.E.,
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99; Conserv
                                       Rodentia;
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21
396 AA;
                                                                                                                                                       PRELIMINARY;
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396
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                                      iinea pig).
  Chordata; Craniata; Vertebrata;
  Hystricognathi; Cavidae; Cavia
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                                                                                        PRECURSOR
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Pred. No. 9e-20;
0; Mismatches 156;
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INTERLEUKIN-5 RECEPTOR TYPE
; 85FBF684 CRC32;
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on update)
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SOLUTION OF THE PROPERTY OF TH
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Query Match
Best Local Similarity 28.0
Matches 89; Conservative
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Best Local Similarity 26.5%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                        Q15469 PRELIMINARY; rn., Q15469; Q15469; Q1-NOV-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NOV-1998 (TrEMBLrel. 08, Last annotation update) SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
                                                                                           SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
MUEDLINE; 92121815.
MURATA Y., TAKAKI S., MIGITA M., KIKUCHI
"MOLECULA" cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and Characterization of the Guinea Pi
receptor alpha cDNA.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ
EMBL; U55215; AAD09361.1;
                                                                                                                                                                       J. Exp. Med. 1
EMBL; X62156;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                     Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---WYEGLDHALQCVDYIKAD-GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEH-KAPPGSPGTSIVNLTCTTNTAASNYTNLKSYEVSLHCTWLAGKDAPEDTQYFLYYR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLNYHVKINTPQEEDYE---TRNTQSKCETTLHQGVSASVRTIL-WH--GHSLLASSWVS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTNA--FYSTTDGVSKYSIQVRAAVSPHCRAMGLWSKWS-QPVYVGKE--KKPIAGWFL
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333 AA;
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28.0%;
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 56; Mismatches
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Pred. No. 1.1e
67; Mismatches
                 Score 292; DB 4;
Pred. No. 3.1e-18;
                                                                                           POTENTIAL.
SOLUBLE INTERLEUKIN-5; E86A7792 CRC32;
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ches 172;
                                                                                                                                                                                                                               Y., TO
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 139;
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an interleukin
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095646;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, I
01-MAY-1999 (TrEMBLrel. 10, I
INTERLEUKIN-13 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORIMASA W., TERUMASA H.; submitted (DCC-1996) to the EMBL/GenBank/DDBJ EMBL; U81379; AAD00510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 WWPWEGAS--SNCSLWYFSHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOPPLELDHEKECTVEY----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHT 107
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     WSNWSQEM-----SIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDP
                                                                                                                                                                                                         KPSFNIVPLTSRVKPDPPHIKNLSFHND---DLYVQWENPQN-FYSRCLFYEVEVNNSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                           LLFWQ: TNGSEVQSSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAAVSSMCREAGLWSEWS 326
                                                                                                                                                                                                                                                         RSSYFTFQLQNIVKPLPP--VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDT 281
                                                                                                                                                                                                                                                                                                                                                          STAWNLFYWYEGIDHALQCVDYIKADGQNIGCRFPYLEASD.-YKDFYICVNGSSENKPI 223
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                                                WSEWSDKQCWEGEDLSKKTLLRFWLPF------GFILILVIFVTGL--LLRKPNTYP
                                                                                                      ETHNVFYVQEAKCENPEFERNVENTS---CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
                                                                                                                                                      T-----LVTATVENETYTLKTTNETRQLCFVV------RSKVNIYC-SDDGI 321
                                                                                                                                                                                                                                                                                                               PRINTELYYMHRSLEKIHQC-ENIFREGQYFGCSFDLTKVKDSSFRQHSVQIMVKDNAGKI
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Pred. No. 4.7e-18;
9; Mismatches 139;
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Best Local :
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                                                                  Q64146 PRELIMINARY: PRT; 896 AA. Q64146; Q14146; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097597
097597;
              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Eutheria; Rodentia; Sciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
NON_TER
NON_TER
SEQUENCE
                                                            RIL-3R<BETA>.
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;
"Biological activities of interleukin-13 on bovine lymphocytes:
implications for signaling through Ir-13Ral.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J- MAY-1999 (TrEMBLrel. 10, Created)
D1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
D1-MAY-1999 (TrEMBLrel. 10, Last sanotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                     VPLTSHVKP-DPSHIKNLSFQNGDLYVQWTNPQN-FQSQCLCYEVEVINSHA-
                                                                                                                                                                                                                                                                                                                                                                                                              YYWHNSLGKILQCENFYR-EGQHIACSFNLTKVKDSSFEQHSVQVMVRDNAGKISPSFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNL 171
                                                                                                                                                                                                                             NWS-----QAMSIGQKANQTFYIT--TLLIIPVIVAAAVI 327
                                                                                                                                                                                                                                                          EWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
                                                                                                                                                                                                                                                                                                                          NETYTLKTTNETR--
                                                                                                                                                                                                                                                                                                                                                                                 FQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                            FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSTNESEKPSILVEKCF-SPPEGDPESAVTALQCIWHNLRYMKCTWLPGRNASPDPNYIL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WNPPEGAS -- PNCSLKY -- - FSHFGNKQDKKIAPET - HRSKEVPLNERICLQVGS -- -- Q 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKIFKEMFGD
                                                                                                                                                                                                                                                                                          -ETHDIFYVEEAKCQNTEFEGNLEGTICFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWS
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83; Conservative
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349
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39644 MW;
           Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.6%;
                                                                                                                                                                                                                                                                                                                     ----QLCFVV------RSKVNIYC-SDDGIWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 264.5; DB 6;
Pred. No. 9.1e-16;
53; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                            Mammalia;
              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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Best Local
CHEN J., GRACE A., CHIEN K.R.;
Submitted (JAN-1998) to the EM
EMBL; AF041845; AAC03531.1; -
PFAM; PF00041; fn3; 4
SEQUENCE 881 AA; 99003 MW;
                                                                                                     Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                          057519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of rat interleukin-3 receptor beta-subunit from icroglia and its mRNA expression in vivo.";
J. Neurosci. 15:5800-5809(1995).
                                                                                                                                                                    01-JUN-1998
01-MAY-1999
                                                                                                                                                                                                             057519;
                                                                  SEQUENCE FROM N.A.
                                                                                                                                               XGP130
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MEDLINE: 95370942.
EPPEL K. BUTTINI M.,
                                                                                                                                                                                               01-JUN-1998
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                                                                                          Kenopus.
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                                                                                                                                                                                                                                                                                       422 EYKGLWSEWSNECTWT-TDWVMPTL---WI----VLILVFLILTFLL
                                                                                                                                                                                                                                                                                                                                                                                               312
                                                                                                                                                                                                                                                                                                                 317 SDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                                                                                                                                                                                                                                                                                                           366 MSYPFIQHAFQVQYKKKLDRWEDSKT----ENLNHAHSMDLPQLEPGTSYCARVRVKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 CSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 LFLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHWDSPTE-DKARPQNLQCFFDGIQSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK 203
                                                                                                                                                                                                                                                                                                                                                                   263 GPIPARCFDYEIEIR-----EDDTTLVTATVENETYTLKTTNETRQLCFVVRSKVNIYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 TLLP-------WQCTNGSEVQ---SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 CVPRRCVLPYTQFSVSKEDYYSLQPDRDLSIHLVVPLAQHVQPPPPKDISISPSG--DHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CSWEVWTKVTDSVSFGLFYSSSPKAGEKKCSPVVKE-----
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87; Conserv
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896 896
896 AA; 99504 MW;
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                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                      PRELIMINARY;
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Last sequence update)
Last annotation updat
                                       EMBL/GenBank/DDBJ databases
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Pred. No. 1.3e-07;
                                                                                                                                                                                                                         PRT;
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                                                                                                     Vertebrata;
ea; Pipidae;
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                                                                                                     Amphibia;
Xenopodinae;
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21;

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Query Match
Best Local Similarity
Matches 88; Conser
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TIEMBLrel. 10, Created)
01-MAY-1999 (TIEMBLrel. 10, Last sequence update)
01-MAY-1999 (TIEMBLREL. 10, Last annotation update)
INTERLEUKIN-5 RECEPTOR BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOGSDON N.J., GRAHAM A., SCOTT C.W.;
"Guinea pig IL5 receptor beta chain.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ
EMBL: U94688; AAC77520.1; -.
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nes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 EYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTLQDLLPNTVYEVSIRC - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LTFTRESSCEIKLKWSIPLGPI------PARCFDYEIEIREDDTTLYTATVENET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YWI-SPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFY-W-YEGLDHALQC 184
                                                                                                                                                                                                                                                                                                                                                  PPQDFEIVDPGYLGYLYLQWQPPLSLDH---FKECTVEYELKYRNIGSETWKTIITKNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTLK-----TTNETRQLCFVVRSKVNIYCSDDGIWSEWSD--KQCW-----EGEDLSKK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELISSLELPNALKIEWKNPITNAFNLKYNIRYRPVKTQDWEM-VPEEDT-----ASHRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYEILNQTTSSVTFENLTTLN----SPLTCNVMASGHV----
                                                   KLKWSIPLGPIPARCF------DYEIEIREDDTTLVTATVENETYTLK-------
                                                                                                                                                                                                 VQDMDCVYYNWQYLLCSWKPGIGVLLLTNYNLFYWYEGLDHALQ-CVDYIKADGQNI---
                                                                                                                                                                                                                                         SNSSQAALGPELFLPSSTYVARVRTRL----ARGSGFSGRPSQWSPEVSWSSQPG-DQAQ
                                                                                                                                                                                                                                                                                                              PPQDVQINTSG--DQVLLTWSVALEGPHTSWLSQRDLEFEVVYKRL-HEPWESAST--LH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CRGANNSCTIHSPGFQFYIDTTFQVEATNELGIQKSETLTIDPVNIVKPNPPQLS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDYIKADGONIGCRE PYLEASDYKDEYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGRPTNLPTNYTLSHRWAHFGANY----
                   SLRW---
                                                                                         HSCQIRVSNPRPHSQYTVTVRPRNGEKFIRSA-----NHIQMAAPT-LNVTKDGD-TY
                                                                                                                            -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEI
                                                                                                                                                                  PQNLQCVFDGAHTLSCSWEVRSQVTSSVSFGLFY-RSSLDAGEQECPQVQKEELHDIYTR
                                                                                                                                                                                                                                                                        -----FDLNKGIEAKIHTLLPWQCTNGSEVQ---SSWAETTYWISPQGIPETK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             890 AA;
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                   VTEKMYYSHIENTFEIQYR---
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25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96579 MW;
                                                                                                                                                                                                                                                                                                                                                                                   8.1%; Score 170; DB 11;
23.8%; Pred. No. 6.8e-07;
tive 53; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Mismatches 115; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EABC43CC CRC32;
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                     -TAGDRWENSKTETLKNAHNMPLPPLEP
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Best Local Similarity
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045561;
01-JUN-1999 (TIZEMBLICEL 06, CI
01-JUN-1998 (TIZEMBLICEL 10, LA
01-MAY:1999 (TIZEMBLICEL 10, LA
PROLACTIN RECEPTOR LONG FORM P
                                                                                                                                               Ovis aries (Sheep). 
Eukaryota; Metazoa; Chordata; Craniata; 
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Jukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Jurheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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01-JAN-1998 (TIEMBLIEL 05, Last sequence update)
01-JAN-1998 (TIEMBLIEL 08, Last annotation update)
PROJACTIN RECEPTOR SHORT FORM.
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^{7}\!\!10^{\circ}.\text{C}_{3} and short forms of the ovine prolactin receptor: cDNA cloning in genomic analysis reveal that the two forms arise by different
                                  SFCTENCE FROM N.A.
MEDLINE; 98001468.
BIGNON C., BINART N.,
SJIANE J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinology 138:3187-3194(1997).
EMBL; AF077403; AAB83999.1; -
PFAM; PF00041; fn3; 2.
SEQUENCE 296 AA; 33854 MW; 8B40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97375450.
SCHULER L.A., MAGEL R.J., GAO J.,
"Prolactin receptor heterogeneity"
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                                                                                                                                                                                                                                                                                                                                                                                        GCFTLVCIRCKPDHGYWSEWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYLWIKWSPPTMTDVKSGWFIIQYVIRLKPEKAT-----DWETHFTLKQTQLKIFNLYP
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Last annotation updat
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Pred. No. 4.7e-07;
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                                                       SCHULER L.A., KELLY P.A.,
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                                                                                                                                                 Pecora; Rovoidea; Bovi
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AC Q9

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Mustela vison (American mink).

Mustela vison (American mink).

Finkaryota; Metazoa; Chordata; Craniata; Vertebrata; Merican mink).

Finkaryota; Metazoa; Chordata; Mustelidae; Mustela
                                                                                                                                                                                                                                                                                                                     046386 PRELIMINARY; PRT; 046386; 01-JUN-1998 (TrembLrel. 06, Created) 01-JUN-1998 (TrembLrel. 06, Last seq 01-MAY-1999 (TrembLrel. 10, Last ann PROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                            NON_TER
                                                                                                                                                                                              DOUGLAS D.A., SONG J.-H., HO Submitted (OCT-1997) to the EMBL; AF029294; AAB88899.1;
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SEQUENCE
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SIGNAL
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Submitted (JAN-1998) to the
EMBL; AF041257; AAB96795.1;
PFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                   TISSUE-TESTIS;
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             216
                                                          158 KPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVN--
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                                                                                     Local Similarity nes 70; Conserv
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                                                                                                                                                                                     PF00041;
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-GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIK------
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217 AA;
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581 AA;
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24850 MW;
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19:109-120(1997).
                                                                                               7.3%;
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he EMBL/GenBank/DDBJ databases
1; -.
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                                                                                   Score 153; DB 6;
Pred. No. 3.7e-06;
86; Mismatches 87
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annotation updat
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RESULT 15
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                   Q16354 PRELIMINARY; PRT; 206 AA. 016354; U1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) PROLACTIN RECEPTOR (FRAGMENT).
                       Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O.,
GATELY M.K., GUBLER U.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; U64198; AAB36675.1; -
PFAM; PF00041; fn3; 3.
SEQUENCE 862 AA; 97134 MW; SFE4FBD5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299665; PRELIMINARY;
299665; Ol-MAY-1997 (TIEMBITEL 03,
01-MAY-1997 (TIEMBITEL 03,
01-NOV-1998 (TIEMBITEL 08,
                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-12 RECEPTOR BETA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 QQISLFW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 LDLKPFYEYEFQISSKLHLY----KGSWSDWSESLRAQTPEEEPTGMLDVWYMKRHIDYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 TKVQDMDCVYYNWQ-YLLCSWKPGIGYLLDTNYNL-----FYWYEGLDHALQCVDYIK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 KPDHGFWSEWSPKRSIQIPNDISMKDTI-VWI---FVAVLSAVICLIMVAAVALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 KNLHYKDGFDLNKGIEAKIHTLLP------WQCTNGSEVQSSWAETTYWISPQGIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 NEMGSSSSDP---RYVT--LTYIVEPDPPVNL----SLELKQPEDKKTYLWIKW-YPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTLLREW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADGONIGCRF-PYLEASDYKDFYICVN--GSSENKPIRSSYFTFQLONIVKPLPP--VYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFQKASVSRCTLYWRDEGLVLLNRLRYRPSNSRLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFTRESSCEIKLKW------SIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRINFHHGHSLNSQV-----TGLPLGTTLFVCKLACINSDEIQICGAEIFVGVAPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-DDGIWSEWSDKQCWE-GEDLSKKTLLRFWLPFGFILIL-----VIFVTGLLLR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLVDVRSGWLTLQYEIRLKPEKAT-----EWETHFAGLQTQFKILSLYPGQKYLVQVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPIPAR----CFDYEIEIREDDTTLVTATVENETYTLKTTNETROLCFVVRSK--VNIYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDK---QCWEGE------DLSK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDYLDFGINLTPESPESNFTAKVTAVNSLGSSSSSLP---STFTF--LDIVRPLPPWDIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QPQNLSCIQKGEQGTVACTWERGRDTHLYTEYTLQLSGPKNLTWQK-----QCKD-IY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 151;
Pred. No. 3.
                                                                     Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHUA A.O., NABAVI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862
                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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Best Local Similarity 27.9
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               cancer cell lin
J. Biol. Chem.
EMBL; S78505; A
PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A MEDLINE; 95286597 FUH G., WELLS J.A
168 KILSLHPGQKYLVQVRCKPDHGYWSAWS 195
                         302 RQLCFVVRSK--VNIYCS-DDGIWSEWS 326
                                                                                                                                                                                                                                          135 IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQN 194
                                                                    114 KOPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPE-----KAAEWEIHFAGQQTEF 167
                                                                                                      255 K-----LKWSIP-LGPIPARCFD--YEIEIREDDTTLVTATVENETYTLKTTNET 301
                                                                                                                                                                           195 IGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prolact
                                                                                                                             61 -SCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPL-----ELAVEV 113
                                                                                                                                                                                                             2 LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHREGETLMHECPDYI-TGGPN 60
                                                                                                                                                                                                                                                                                                                                                                  206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    270:13133-13137(1995).
AAB34470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonists that inhibit the growth of breast
                                                                                                                                                                                                                                                                                                                                                                23950 MW; L7E57266 CRC32;
                                                                                                                                                                                                                                                                            7.2%; Score 151; DB 4; Length 206; 27.9%; Pred. No. 5.2e-06; tive 26; Mismatches 94; Indels
                                                                                                                                                                                                                                                                              30; Gaps
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Search completed: January 20, 2000, 06:37:46 Job time: 1004 sec

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